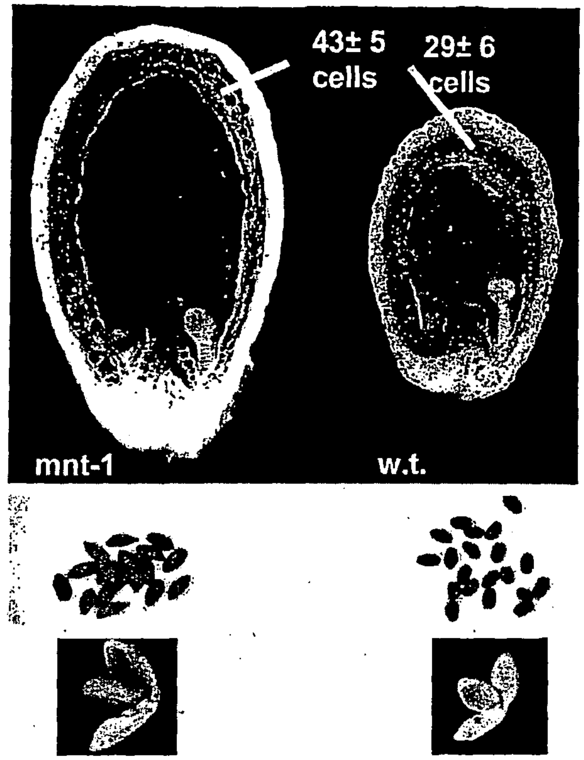
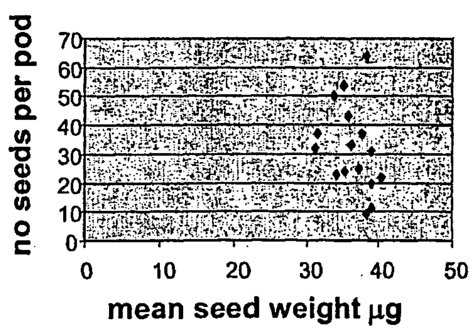
Figure 1

1A mnt-1 vs wild-type seeds



1B Seed weight vs no. seeds per pod in mnt-1



1C Maternal effect of mnt-1 mutation

mnt-1
seed parent

w.t.
seed parent

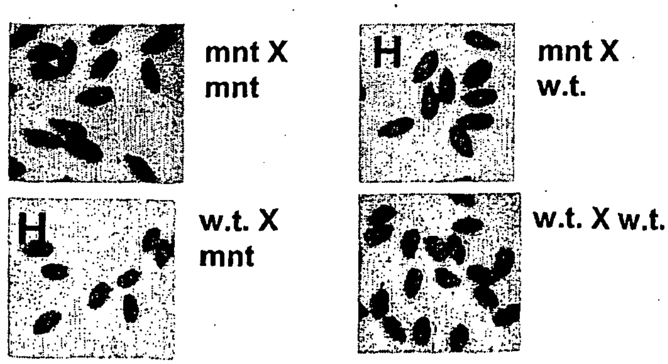
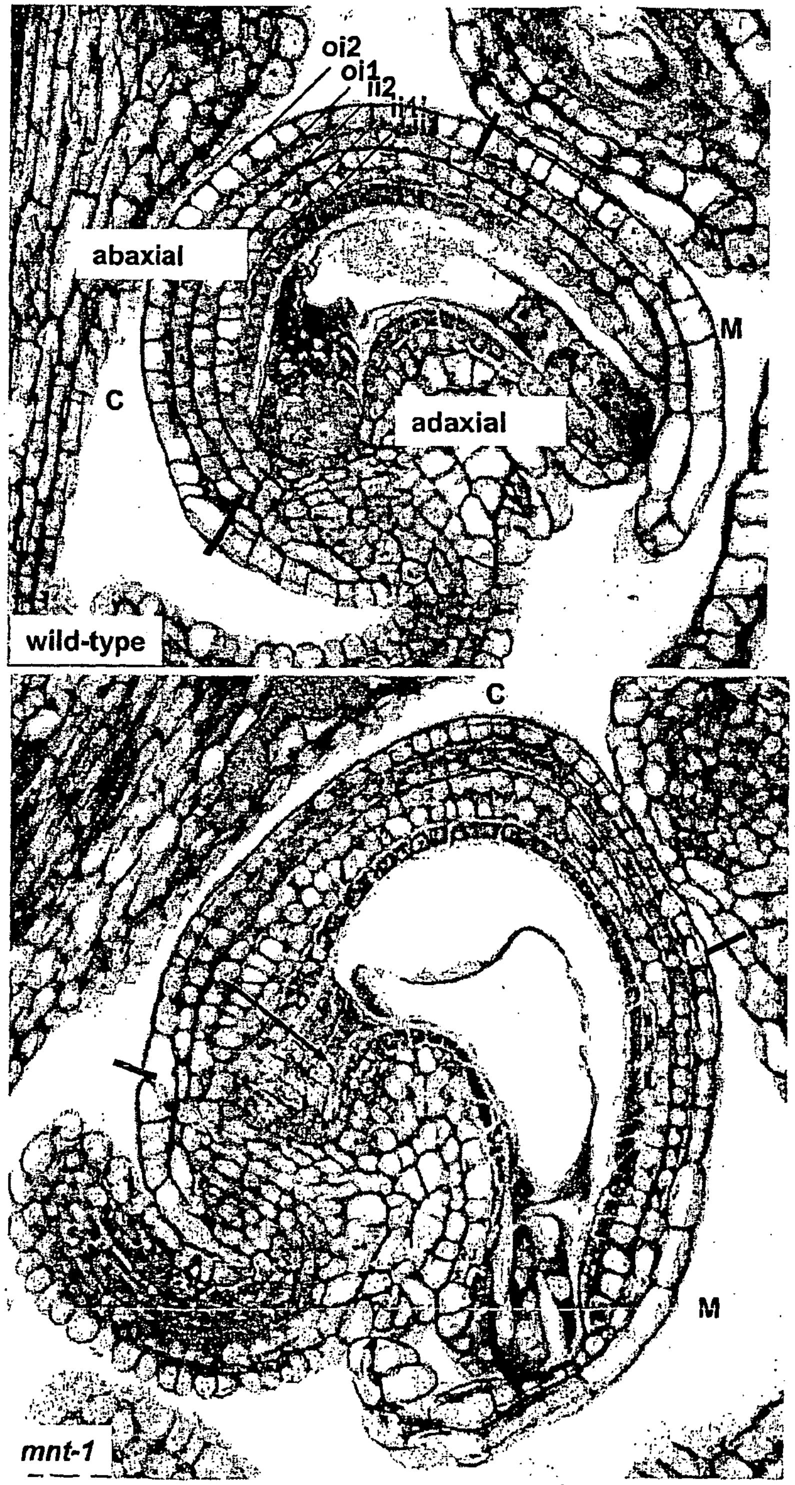


Figure 2

2A Mature w.t. and mnt-1 ovules



2B Cell number and size in w.t. and mnt-1 integuments

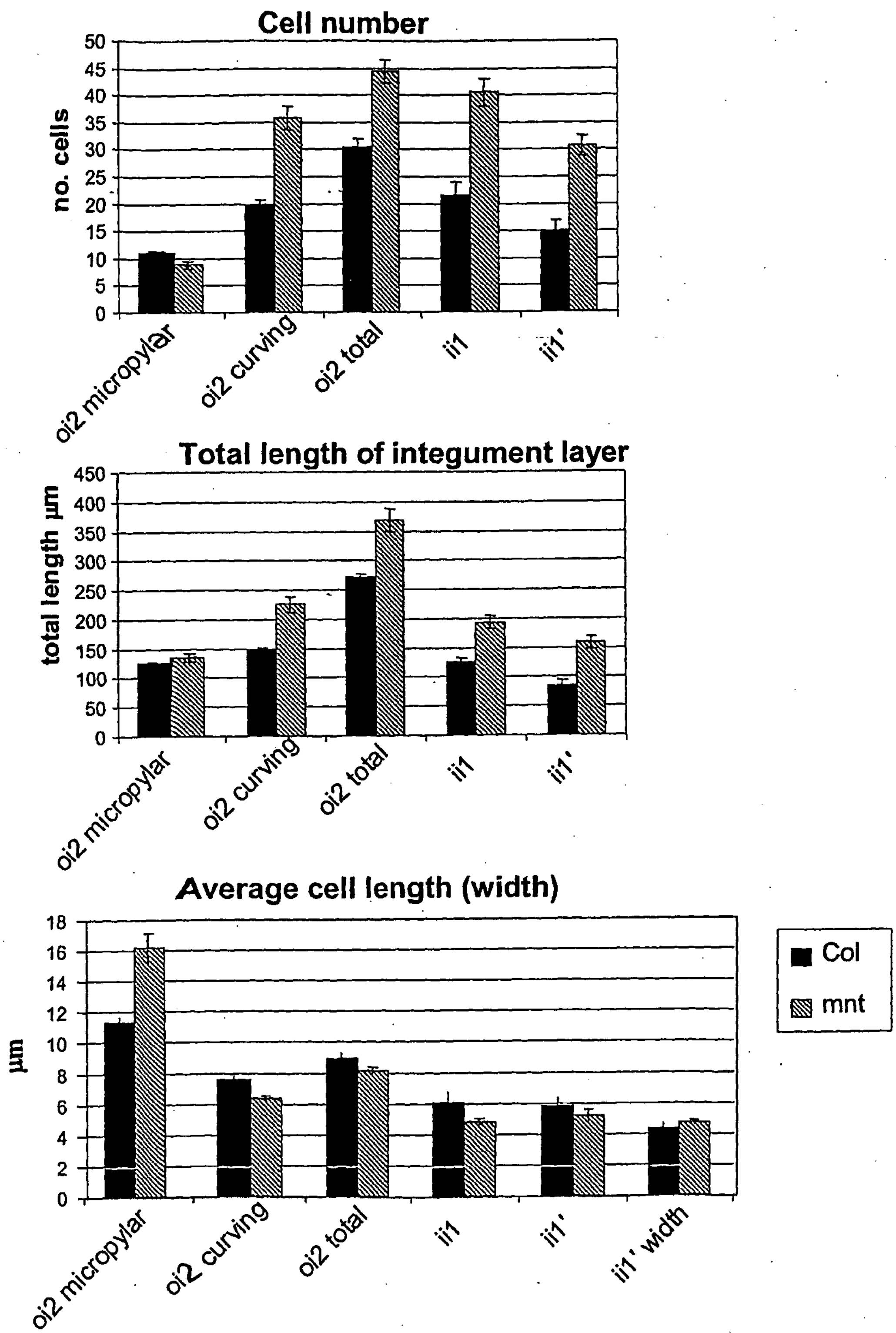
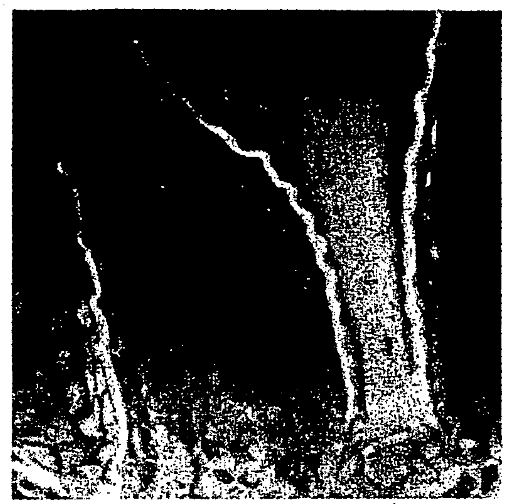


Figure 3
Chalazal endosperm

w.t. 7DAP



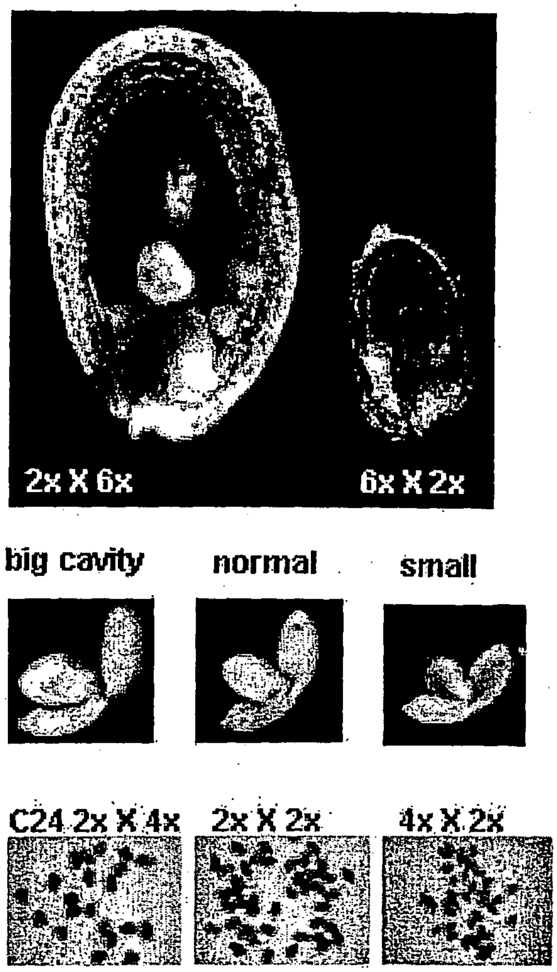
mnt-1 7DAP

2x X 6x 5 DAP

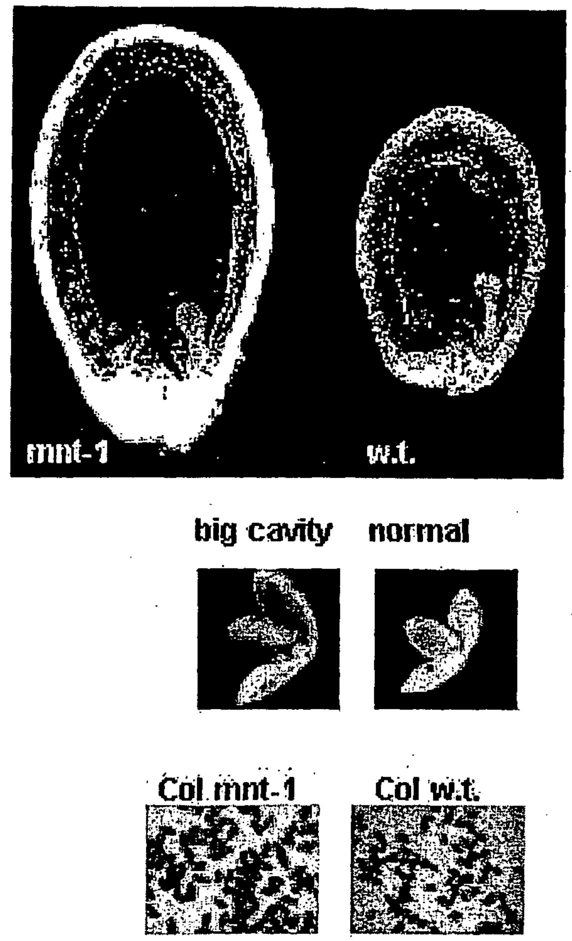
Bars = 50 μm

Figure 4

4A Endosperm-led growth



4B Integument-led growth



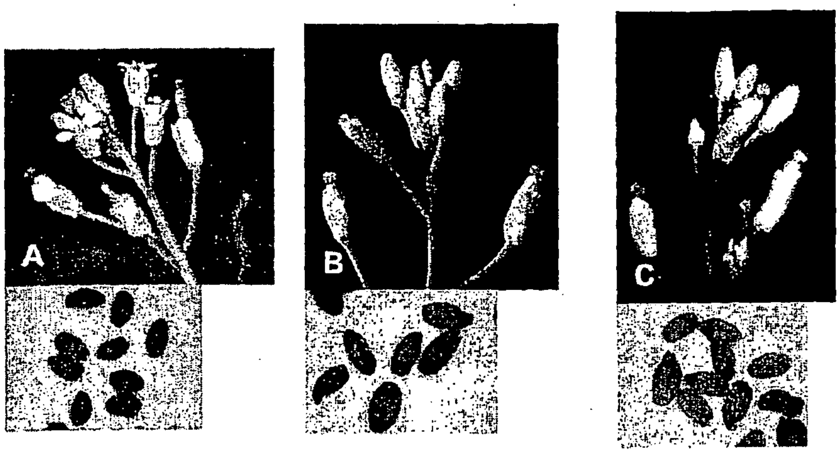
4C 'Big bag' hypothesis: seed and embyro size set by size of the seed cavity

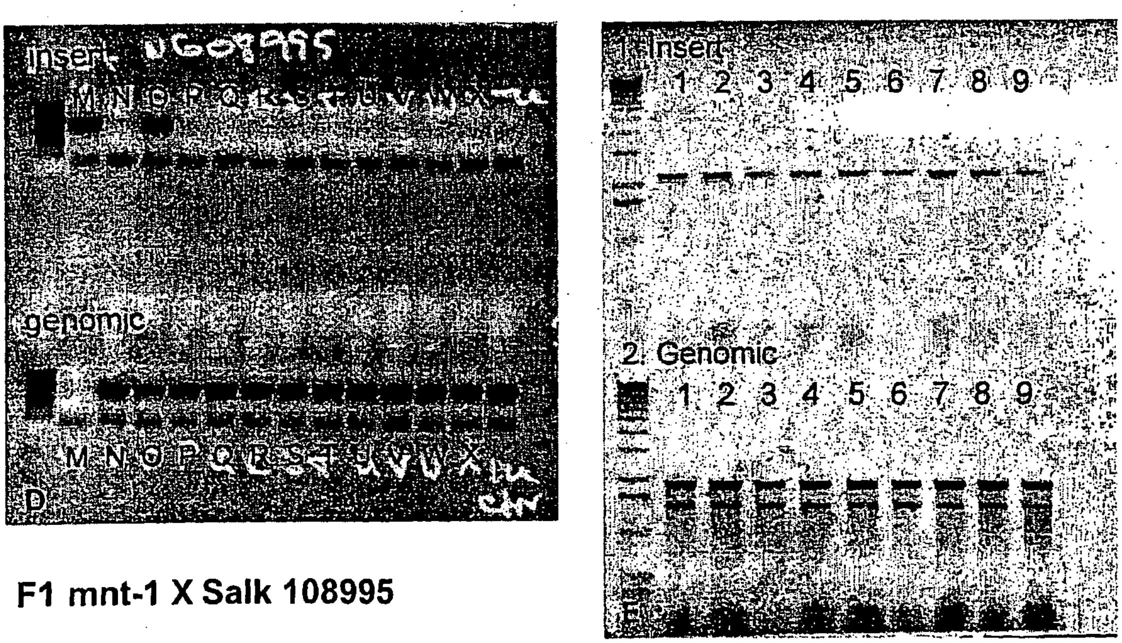
1. Division in endosperm (maternal and paternal control)
2. Division in integuments/ seed coat (maternal control)

Figure 5

Allelism of mnt-1 and Salk insertion line 108995

Col-3 w.t. **mnt-1** **Salk 108995 homozygote**





F1 mnt-1 X Salk 108995

Figure 6

Alignment of w.t. MNT and mutant mnt-1 cDNA

```
MNT           *        20          *        40          *        60
ATGGCGAGTTCGGAGGTTTCAATGAAAGGTAATCGTGGAGGAGATAACTTCTCCTCCTCT
ATGGCGAGTTCGGAGGTTTCAATGAAAGGTAATCGTGGAGGAGATAACTTCTCCTCCTCT
mnt-1

              *        80          *       100          *       120
GGTTTTAGTGACCCTAAGGAGACTAGAAATGTCTCCGTCGCCGGCGAGGGGCAAAAAAGT
GGTTTTAGTGACCCTAAGGAGACTAGAAATGTCTCCGTCGCCGGCGAGGGGCAAAAAAGT

              *       140          *       160          *       180
AATTCTACCCGATCCGCTGCGGCTGAGCGTGCTTTGGACCCTGAGGCTGCTCTTTACAGA
AATTCTACCCGATCCGCTGCGGCTGAGCGTGCTTTGGACCCTGAGGCTGCTCTTTACAGA

              *       200          *       220          *       240
GAGCTATGGCACGCTTGTGCTGGTCCGCTTGTGACGGTTCCTAGACAAGACGACCGAGTC
GAGCTATGGCACGCTTGTGCTGGTCCGCTTGTGACGGTTCCTAGACAAGACGACCGAGTC

              *       260          *       280          *       300
TTCTATTTTCCTCAAGGACACATCGAGCAGGTGGAGGCTTCGACGAACCAGGCGGCAGAA
TTCTATTTTCCTCAAGGACACATCGAGCAGGTGGAGGCTTCGACGAACCAGGCGGCAGAA

              *       320          *       340          *       360
CAACAGATGCCTCTCTATGATCTTCCGTCAAAGCTTCTCTGTCGAGTTATTAATGTAGAT
CAACAGATGCCTCTCTATGATCTTCCGTCAAAGCTTCTCTGTCGAGTTATTAATGTAGAT

              *       380          *       400          *       420
TTAAAGGGAGAGGCAGATACAGATGAAGTTTATGCGCAGATTACTCTTCTTCCTGAGGCT
TTAAAG----AGGCAGATACAGATGAAGTTTATGCGCAGATTACTCTTCTTCCTGAGGCT

              *       440          *       460          *       480
AATCAAGACGAGAATGCAATTGAGAAAGAAGCGCCTCTTCCTCCACCTCCGAGGTTCCAG
AATCAAGACGAGAATGCAATTGAGAAAGAAGCGCCTCTTCCTCCACCTCCGAGGTTCCAG

              *       500          *       520          *       540
GTGCATTCGTTCTGCAAAACCTTGACTGCATCCGACACAAGTACACATGGTGGATTTTCT
GTGCATTCGTTCTGCAAAACCTTGACTGCATCCGACACAAGTACACATGGTGGATTTTCT
```

* 560 * 580 * 600

GTTCTTAGGCGACATGCGGATGAATGTCTCCCACCTCTGGATATGTCTCGACAGCCTCCC
GTTCTTAGGCGACATGCGGATGAATGTCTCCCACCTCTGGATATGTCTCGACAGCCTCCC

* 620 * 640 * 660

ACTCAAGAGTTAGTTGCAAAGGATTTGCATGCAAATGAGTGGCGATTCAGACATATATTC
ACTCAAGAGTTAGTTGCAAAGGATTTGCATGCAAATGAGTGGCGATTCAGACATATATTC

* 680 * 700 * 720

CGGGGTCAACCACGGAGGCATTTGCTACAGAGTGGGTGGAGTGTGTTTGTTAGCTCCAAA
CGGGGTCAACCACGGAGGCATTTGCTACAGAGTGGGTGGAGTGTGTTTGTTAGCTCCAAA

* 740 * 760 * 780

AGGCTAGTTGCAGGCGATGCGTTTATATTTCTAAGGGGCGAGAATGGAGAATTAAGAGTT
AGGCTAGTTGCAGGCGATGCGTTTATATTTCTAAGGGGCGAGAATGGAGAATTAAGAGTT

* 800 * 820 * 840

GGTGTAAGGCGTGCGATGCGACAACAAGGAAACGTGCCGTCTTCTGTTATATCTAGCCAT
GGTGTAAGGCGTGCGATGCGACAACAAGGAAACGTGCCGTCTTCTGTTATATCTAGCCAT

* 860 * 880 * 900

AGCATGCATCTTGGAGTACTGGCCACCGCATGGCATGCCATTTCAACAGGGACTATGTTT
AGCATGCATCTTGGAGTACTGGCCACCGCATGGCATGCCATTTCAACAGGGACTATGTTT

* 920 * 940 * 960

ACAGTCTACTACAAACCCAGGACGAGCCCATCTGAGTTTATTGTTCCGTTCGATCAGTAT
ACAGTCTACTACAAACCCAGGACGAGCCCATCTGAGTTTATTGTTCCGTTCGATCAGTAT

* 980 * 1000 * 1020

ATGGAGTCTGTTAAGAATAACTACTCTATTGGCATGAGATTCAAAATGAGATTTGAAGGC
ATGGAGTCTGTTAAGAATAACTACTCTATTGGCATGAGATTCAAAATGAGATTTGAAGGC

* 1040 * 1060 * 1080

GAAGAGGCTCCTGAGCAGAGGTTTACTGGCACAATCGTTGGGATTGAAGAGTCTGATCCT
GAAGAGGCTCCTGAGCAGAGGTTTACTGGCACAATCGTTGGGATTGAAGAGTCTGATCCT

* 1100 * 1120 * 1140

ACTAGGTGGCCAAAATCAAAGTGGAGATCCCTCAAGGTGAGATGGGATGAGACTTCTAGT
ACTAGGTGGCCAAAATCAAAGTGGAGATCCCTCAAGGTGAGATGGGATGAGACTTCTAGT

```
           *        1160         *        1180         *        1200
ATTCCTCGACCTGATAGAGTATCTCCGTGGAAAGTAGAGCCAGCTCTTGCTCCTCCTGCT
ATTCCTCGACCTGATAGAGTATCTCCGTGGAAAGTAGAGCCAGCTCTTGCTCCTCCTGCT

           *        1220         *        1240         *        1260
TTGAGTCCTGTTCCAATGCCTAGGCCTAAGAGGCCCAGATCAAATATAGCACCTTCATCT
TTGAGTCCTGTTCCAATGCCTAGGCCTAAGAGGCCCAGATCAAATATAGCACCTTCATCT

           *        1280         *        1300         *        1320
CCTGACTCTTCGATGCTTACCAGAGAAGGTACAACTAAGGCAAACATGGACCCTTTACCA
CCTGACTCTTCGATGCTTACCAGAGAAGGTACAACTAAGGCAAACATGGACCCTTTACCA

           *        1340         *        1360         *        1380
GCAAGCGGACTTTCAAGGGTCTTGCAAGGTCAAGAATACTCGACCTTGAGGACGAAACAT
GCAAGCGGACTTTCAAGGGTCTTGCAAGGTCAAGAATACTCGACCTTGAGGACGAAACAT

           *        1400         *        1420         *        1440
ACTGAGAGTGTAGAGTGTGATGCTCCTGAGAATTCTGTTGTCTGGCAATCTTCAGCGGAT
ACTGAGAGTGTAGAGTGTGATGCTCCTGAGAATTCTGTTGTCTGGCAATCTTCAGCGGAT

           *        1460         *        1480         *        1500
GATGATAAGGTTGACGTGGTTTCGGGTTCTAGAAGATATGGATCTGAGAACTGGATGTCC
GATGATAAGGTTGACGTGGTTTCGGGTTCTAGAAGATATGGATCTGAGAACTGGATGTCC

           *        1520         *        1540         *        1560
TCAGCCAGGCATGAACCTACTTACACAGATTTGCTCTCCGGCTTTGGGACTAACATAGAT
TCAGCCAGGCATGAACCTACTTACACAGATTTGCTCTCCGGCTTTGGGACTAACATAGAT

           *        1580         *        1600         *        1620
CCATCCCATGGTCAGCGGATACCTTTTTATGACCATTCATCATCACCTTCTATGCCTGCA
CCATCCCATGGTCAGCGGATACCTTTTTATGACCATTCATCATCACCTTCTATGCCTGCA

           *        1640         *        1660         *        1680
AAGAGAATCTTGAGTGATTCAGAAGGCAAGTTCGATTATCTTGCTAACCAGTGGCAGATG
AAGAGAATCTTGAGTGATTCAGAAGGCAAGTTCGATTATCTTGCTAACCAGTGGCAGATG

           *        1700         *        1720         *        1740
ATACACTCTGGTCTCTCCCTGAAGTTACATGAATCTCCTAAGGTACCTGCAGCAACTGAT
ATACACTCTGGTCTCTCCCTGAAGTTACATGAATCTCCTAAGGTACCTGCAGCAACTGAT
```

```
           *       1760         *       1780         *       1800
GCGTCTCTCCAAGGGCGATGCAATGTTAAATACAGCGAATATCCTGTTCTTAATGGTCTA
GCGTCTCTCCAAGGGCGATGCAATGTTAAATACAGCGAATATCCTGTTCTTAATGGTCTA

           *       1820         *       1840         *       1860
TCGACTGAGAATGCTGGTGGTAACTGGCCAATACGTCCACGTGCTTTGAATTATTATGAG
TCGACTGAGAATGCTGGTGGTAACTGGCCAATACGTCCACGTGCTTTGAATTATTATGAG

           *       1880         *       1900         *       1920
GAAGTGGTCAATGCTCAAGCGCAAGCTCAGGCTAGGGAGCAAGTAACAAAACAACCCTTC
GAAGTGGTCAATGCTCAAGCGCAAGCTCAGGCTAGGGAGCAAGTAACAAAACAACCCTTC

           *       1940         *       1960         *       1980
ACGATACAAGAGGAGACAGCAAAGTCAAGAGAAGGGAACTGCAGGCTCTTTGGCATTCCT
ACGATACAAGAGGAGACAGCAAAGTCAAGAGAAGGGAACTGCAGGCTCTTTGGCATTCCT

           *       2000         *       2020         *       2040
CTGACCAACAACATGAATGGGACAGACTCAACCATGTCTCAGAGAAACAACTTGAATGAT
CTGACCAACAACATGAATGGGACAGACTCAACCATGTCTCAGAGAAACAACTTGAATGAT

           *       2060         *       2080         *       2100
GCTGCGGGGCTTACACAGATAGCATCACCAAAGGTTCAGGACCTTTCAGATCAGTCAAAA
GCTGCGGGGCTTACACAGATAGCATCACCAAAGGTTCAGGACCTTTCAGATCAGTCAAAA

           *       2120         *       2140         *       2160
GGGTCAAAATCAACAAACGATCATCGTGAACAGGGAAGACCATTCCAGACTAATAATCCT
GGGTCAAAATCAACAAACGATCATCGTGAACAGGGAAGACCATTCCAGACTAATAATCCT

           *       2180         *       2200         *       2220
CATCCGAAGGATGCTCAAACGAAAACCAACTCAAGTAGGAGTTGCACAAAGGTTCACAAG
CATCCGAAGGATGCTCAAACGAAAACCAACTCAAGTAGGAGTTGCACAAAGGTTCACAAG

           *       2240         *       2260         *       2280
CAGGGAATTGCACTTGGCCGTTCAGTGGATCTTTCAAAGTTCCAAAACTATGAGGAGTTA
CAGGGAATTGCACTTGGCCGTTCAGTGGATCTTTCAAAGTTCCAAAACTATGAGGAGTTA

           *       2300         *       2320         *       2340
GTCGCTGAGCTGGACAGGCTGTTTGAGTTCAATGGAGAGTTGATGGCTCCTAAGAAAGAT
GTCGCTGAGCTGGACAGGCTGTTTGAGTTCAATGGAGAGTTGATGGCTCCTAAGAAAGAT
```

```
                 *       2360         *       2380         *       2400
TGGTTGATAGTTTACACAGATGAAGAGAATGATATGATGCTTGTTGGTGACGATCCTTGG
TGGTTGATAGTTTACACAGATGAAGAGAATGATATGATGCTTGTTGGTGACGATCCTTGG

                 *       2420         *       2440         *       2460
CAGGAGTTTTGTTGCATGGTTCGCAAAATCTTCATATACACGAAAGAGGAAGTGAGGAAG
CAGGAGTTTTGTTGCATGGTTCGCAAAATCTTCATATACACGAAAGAGGAAGTGAGGAAG

                 *       2480         *       2500         *       2520
ATGAACCCGGGGACTTTAAGCTGTAGGAGCGAGGAAGAAGCAGTTGTTGGGGAAGGATCA
ATGAACCCGGGGACTTTAAGCTGTAGGAGCGAGGAAGAAGCAGTTGTTGGGGAAGGATCA

                 *       2540         *       2560         *       2580
GATGCAAAGGACGCCAAGTCTGCATCAAATCCTTCATTGTCCAGCGCTGGGAACTCTTAA
GATGCAAAGGACGCCAAGTCTGCATCAAATCCTTCATTGTCCAGCGCTGGGAACTCTTAA
```

Figure 7

Alignment of w.t. MNT and mutant mnt-1 protein

```
MNT        *         20         *         40         *         60
MASSEVSMKGNRGGDNFSSSGFSDPKETRNVSVAGEGQKSNSTRSAAAERALDPEAALYR
MASSEVSMKGNRGGDNFSSSGFSDPKETRNVSVAGEGQKSNSTRSAAAERALDPEAALYR
mnt-1

           *         80         *        100         *        120
ELWHACAGPLVTVPRQDDRVFYFPQGHIEQVEASTNQAAEQQMPLYDLPSKLLCRVINVD
ELWHACAGPLVTVPRQDDRVFYFPQGHIEQVEASTNQAAEQQMPLYDLPSKLLCRVINVD

           *        140         *        160         *        180
LKAEADTDEVYAQITLLPEANQDENAIEKEAPLPPPPRFQVHSFCKTLTASDTSTHGGES
LKRQIQMKFMRRLLFFLRLIKTRMQLRKKRLFLHLRGSRCIRSAKP--------------

           *        200         *        220         *        240
VLRRHADECLPPLDMSRQPPTQELVAKDLHANEWRFRHIFRGQPRRHLLQSGWSVFVSSK
------------------------------------------------------------

           *        260         *        280         *        300
RLVAGDAFIFLRGENGELRVGVRRAMRQQGNVPSSVISSHSMHLGVLATAWHAISTGTME
------------------------------------------------------------

           *        320         *        340         *        360
TVYYKPRTSPSEFIVPFDQYMESVKNNYSIGMRFKMRFEGEEAPEQRFTGTIVGIEESDP
------------------------------------------------------------

           *        380         *        400         *        420
TRWPKSKWRSLKVRWDETSSIPRPDRVSPWKVEPALAPPALSPVPMPRPKRPRSNIAPSS
------------------------------------------------------------

           *        440         *        460         *        480
PDSSMLTREGTTKANMDPLPASGLSRVLQGQEYSTLRTKHTESVECDAPENSVVWQSSAD
------------------------------------------------------------

           *        500         *        520         *        540
DDKVDVVSGSRRYGSENWMSSARHEPTYTDLLSGFGTNIDPSHGQRIPFYDHSSSPSMPA
------------------------------------------------------------

           *        560         *        580         *        600
KRILSDSEGKFDYLANQWQMIHSGLSLKLHESPKVPAATDASLQGRCNVKYSEYPVLNGL
------------------------------------------------------------
```

```
         *         620         *         640         *         660
STENAGGNWPIRPRALNYYEEVVNAQAQAQAREQVTKQPFTIQEETAKSREGNCRLFGIP
------------------------------------------------------------

         *         680         *         700         *         720
LTNNMNGTDSTMSQRNNLNDAAGLTQIASPKVQDLSDQSKGSKSTNDHREQGRPFQTNNP
------------------------------------------------------------

         *         740         *         760         *         780
HPKDAQTKTNSSRSCTKVHKQGIALGRSVDLSKFQNYEELVAELDRLFEFNGELMAPKKD
------------------------------------------------------------

         *         800         *         820         *         840
WLIVYTDEENDMMLVGDDPWQEFCCMVRKIFIYTKEEVRKMNPGTLSCRSEEEAVVGEGS
------------------------------------------------------------

         *
DAKDAKSAASNPSLSSAGNS
--------------------
```

Figure 8
Alignment of MNT and BnARF2 cDNA

```
MNT
                  *        20         *        40         *        60
ATGGCGAGTTCGGAGGTTTCAATGAAAGGTAATCGTGGA---GGAGATAACTTCTCCTCC
ATGGCGAGTTCGGAGGTTTCTATGAAAGGAAATCGTGGACGAGGAGAAAACTTCTCCTCC
BnARF2
                  *        80         *       100         *       120
TCTGGTTTTAGTGACCCTAAGGAGACTAGAAATGTCTCCGTCGCCGGCGAGGGGCAAAAA
GCTGGTTACAGTGACCC------GAC--------G-----GTCGCCGGCGAGGCGCAGAAA

                  *       140         *       160         *       180
AGTAATTCTACCCGATCGGCTGCGGCTGAGCGTGCTTTGGACCCTGAGGCTGCTCTTTAC
AGTCAGTCTAACCGATCTGTGGCTGCAGAGCGCGTTGTCGACCCGGAAGCTGCTCTCTAC

                  *       200         *       220         *       240
AGAGAGCTATGGCACGCTTGTGCTGGTCCGCTTGTGACGGTTCCTAGACAAGACGACCGA
CGTGAGCTGTGGCACGCTTGTGCTGGTCCTCTCGTGACAGTCCCTCGACAAGATGACCGA

                  *       260         *       280         *       300
GTCTTCTATTTTCCTCAAGGACACATCGAGCAGGTGGAGGCTTCGACGAACCAGGCGGCA
GTCTTCTACTTCCCTCAGGGGCACATCGAGCAGGTGGAAGCATCGACAAATCAAGCTGCA

                  *       320         *       340         *       360
GAACAACAGATGCCTCTCTATGATCTTCCGTCAAAGCTTCTCTGTCGAGTTATTAATGTA
GAACAGCAGATGCCTCTCTATGATCTTCCTTCGAAGATCCTTTGTCGTGTCATTAATGTT

                  *       380         *       400         *       420
GATTTAAAGGCAGAGGCAGATACAGATGAAGTTTATGCGCAGATTACTCTTCTTCCTGAG
GATTTAAAGGCAGAGGCAGACACCGACGAAGTTTATGCGCAGATTACTCTTCTTCCGGAG

                  *       440         *       460         *       480
GCTAATCAAGACGAGAATGCAATTGAGAAAGAAGCGCCTCTTCCTCCACCTCCGAGGTTC
CCTGTTCAAGACGAGAATTCAATAGAGAAAGACGCGCCTCCTCCTCCGCCCCCAAGGTTC

                  *       500         *       520         *       540
CAGGTGCATTCGTTCTGCAAAACCTTGACTGCATCCGACACAAGTACACATGGTGGATTT
CAAGTGCACTCCTTCTGCAAAACCTTGACTGCATCGGACACAAGTACACATGGTGGATTT
```

```
                 *      560           *      580           *      600
TCTGTTCTTAGGCGACATGCGGATGAATGTCTCCCACCTCTGGATATGTCTCGACAGCCT
TCTGTGCTTAGGCGGCATGCGGATGAATGTCTCCCACCTCTGGATATGTCACGTCAACCT

                 *      620           *      640           *      660
CCGACTCAAGAGTTAGTTGCAAAGGATTTGCATGCAAATGAGTGGCGATTCAGACATATA
CCTACTCAGGAGTTAGTTGCAAAAGATGTGCATGCAAGCGAGTGGCGTTTCCGACATATT

                 *      680           *      700           *      720
TTCCGGGGTCAACCACGGAGGCATTTGCTACAGAGTGGGTGGAGTGTGTTTGTTAGCTCC
TTCCGAGGTCAACCACGAAGGCATTTGCTTCAGAGTGGATGGAGCGTGTTTGTTAGCTCC

                 *      740           *      760           *      780
AAAAGGCTAGTTGCAGGCGATGCGTTTATATTTCTAAGGGGCGAGAATGGAGAATTAAGA
AACAGGCTGGTGGCAGGCGATGCTTTTATATTTCTAAGGGGCGAGAATGGAGAATTACGT

                 *      800           *      820           *      840
GTTGGTGTAAGGCGTGCGATGCGACAACAAGGAAACGTGCCGTCTTCTGTTATATCTAGC
GTGGGTGTAAGGCGTGCAATGCGGCAGCAAGGAAATGTGCCATCCTCTGTTATATCAAGC

                 *      860           *      880           *      900
CATAGCATGCATCTTGGAGTACTGGCCACCGCATGGCATGCCATTTCAACAGGGACTATG
CACAGCATGCATCTCGGAGTATTGGCCACTGCCTGGCACGCTATTTCAACTGGAACCATG

                 *      920           *      940           *      960
TTTACAGTCTACTACAAACCCAGGACGAGCCCATCTGAGTTTATTGTTCCGTTCGATCAG
TTTACAGTCTACTATAAACCGAGGACTAGTCCTTCAGAGTTTATTGTTCCGTTTGATCAG

                 *      980           *     1000           *     1020
TATATGGAGTCTGTTAAGAATAACTACTCTATTGGCATGAGATTCAAAATGAGATTTGAA
TATACGGAGTCCGTGAAGATTAACTACTCCATAGGCATGAGATTTAAAATGAGATTTGAA

                 *     1040           *     1060           *     1080
GGCGAAGAGGCTCCTGAGCAGAGGTTTACTGGCACAATCGTTGGGATTGAAGAGTCTGAT
GGCGAAGAGGCTCCCGAGCAGAGGTTTACTGGCACAATCGTTGGGATTGAAGACTCTGAC

                 *     1100           *     1120           *     1140
CCTACTAGGTGGCCAAAATCAAAGTGGAGATCCCTCAAGGTGAGATGGGATGAGACTTCT
CCCACGAGGTGGGCAAAATCAAAATGGAGATCCCTCAAGGTACGGTGGGATGAGACCACT
```

```
         *      1160         *      1180         *      1200
AGTATTCCTCGACCTGATAGAGTATCTCCGTGGAAAGTAGAGCCAGCTCTTGCTCCTCCT
AGTATTCCTCGCCCTGATAGAGTATCCCCGTGGAAGATAGAGCCAGCTCTTTCTCCTCCT

         *      1220         *      1240         *      1260
GCTTTGAGTCCTGTTCCAATGCCTAGGCCTAAGAGGCCCAGATCAAATATAGCACCTTCA
GCTTTGAGCCCTGTACCAATGCCTAGGCCTAAGAGGCCCAGATCTAATCTAGCTTCTTCA

         *      1280         *      1300         *      1320
TCTCCTGACTCTTCGATGCTTACCAGAGAAGGTACAACTAAGGCAAACATGGACCCTTTA
ACTCCGGACTCTTCCATGCGCATAAGGGAAGGCTCATCTAAGGCAAACATGGACCCTTTA

         *      1340         *      1360         *      1380
CCAGCAAGCGGACTTTCAAGGGTCTTGCAAGGTCAAGAATACTCGACCTTGAGGACGAAA
CCGGCAAGTGGACTATCAAGGGTCTTGCAAGGTCAAGAATACCCGACCTTGAGAACGAAA

         *      1400         *      1420         *      1440
CATACTGAGAGTGTAGAGTGTGATGCTCCTGAGAATTCTGTTGTCTGGCAATCTTCAGCG
CATGTTGAGAGTGTAGAATGCGATGCTCCTGAAAATTCGGTTGTGTGGCAATCGTCAACT

         *      1460         *      1480         *      1500
GATGATGATAAGGTTGACGTGGTTTCGGCTTCTAGAAGATATGGATCTGAGAACTGGATG
GATGATGACAAGGTTGATGTGATTTCAGCTTCTAGGAGATATG------AGAACTGGATA

         *      1520         *      1540         *      1560
TCCTCAGCCAGGCATGAACCTACTTACACAGATTTGCTCTCCGGCTTTGGGACTAACATA
TCCTCAGGTAGGCATGGACCTACTTGCACGGATTTGCTTTCTGGCTTTGGGACAAACATA

         *      1580         *      1600         *      1620
GATCCATCCCATGGTCAGCGGATACCTTTTTATGACCATT---CATCATCACCTTCTATG
GAACCACCTCACGGTCATCAGATACCTTTTTATGACCGTTTATCATCAGCACCTTCTGTG

         *      1640         *      1660         *      1680
GCTGCAAAGAGAATCTTGAGTGATTCAGAAGGCAAGTTCGATTATCTTGCTAACCAGTGG
GCTGCAAGGAAAATCCTCAGCGACCAGGATGGCAAGTTTGAATATCTTGCTAACCAGTGG

         *      1700         *      1720         *      1740
CAGATGATACACTCTGGTCTCTCCCTGAAGTTACATGAATCTCCTAAGGTACCTGCAGCA
---ATGATGCACTCAGGCCTTTCCCTGAAGTTACATGAATCTCCTAAAGTCCCTGCCGCA
```

```
          *       1760          *       1780          *       1800
ACTGATGCGTCTCTCCAAGGGCGATGCAATGTTAAATACAGCGAATATCCTGTTCTTAAT
TCTGATGCCTCTTTCCAAGGGATAGGCAATGCCAATTACGGCGAATATGCTTTGCCTCGT

          *       1820          *       1840          *       1860
GGTCTATCGACTGAGAATGCTGGTGGTAACTGGCCAATACGTCCACGTGCTTTGAATTAT
GCAGTGACGACTGAGAATGCTGCTGGCAACTGGCCAATACGTCCACGTGCTCTAAATTAT

          *       1880          *       1900          *       1920
TATGAGGAAGTGGTCAATGCTCAAGCGCAAGCTCAGGCTAGGGAGCAAGTAACAAAACAA
TTTGAAGAAGCGGT------TCAT------GCTCAGGCTAGAGAGCATGTGACAAAACGT

          *       1940          *       1960          *       1980
CCCTTCA--CGATACAAGAGGAGACAGCAAAGTCAAGAGAAGGGAACTGCAGGCTCTTTG
CC-TGCGGTCG-TACAAGAGGAGGCAGCAAAGCCAAGAGACGGGAACTGCAGGCTTTTTG

          *       2000          *       2020          *       2040
GCATTCCTCTGACCAACAACATGAATGGGACAGACTCAACGATGTCTCAGAGAAACAACT
GCATTCCTCTGGTGAACAACGTGAATGGGACAGATACAACTTTGTCTCAGAGAAACAATT

          *       2060          *       2080          *       2100
TGAATGATGCTGCGGGGCTTACACAGATAGCATCACCAAAGGTTCAGGACCTTTCAGATC
TGAATGACCCTGCGGGGCCTACGCAGATGGCATCACCAAAGGTTCAGGATCTTTCTGACC

          *       2120          *       2140          *       2160
AGTCAAAAGGGTCAAAATCAACAAACGATCATCGTGAACAGGGAAGACCATTCCAGACTA
AGTCCAAAGGGTCAAAATCGACAAATGATCATCGTGAGCAAGGACGACCATTCCCGGTTA

          *       2180          *       2200          *       2220
ATAATCCTCATCCGAAGGATGCTCAAACGAAAACCAACTCAAGTAGGAGTTGCACAAAGG
GTAAACCCCATCCGAAAGACGTTCAAACCAAAACAAACTCATGTAGGAGCTGCACGAAGG

          *       2240          *       2260          *       2280
TTCACAAGCAGGGAATTGCACTTGGCCGTTCAGTGGATCTTTCAAAGTTCCAAAACTATG
TTCAGAAGCAGGGGATTGCACTTGGCCGGTCAGTGGATCTCTCAAAGTTCCAGAACTATG

          *       2300          *       2320          *       2340
AGGAGTTAGTCGCTGAGCTGGACAGGCTGTTTGAGTTCAATGGAGAGTTGATGGCTCCTA
AGGAGTTGGTTACTGAATTGGATAGGCTGTTTGAGTTCAATGGAGAGTTGATGGCTCCTA
```

```
          *       2360         *       2380          *       2400
AGAAAGATTGGTTGATAGTTTACACAGATGAAGAGAATGATATGATGCTTGTTGGTGACG
AGAAAGATTGGCTGATAGTTTACACAGATGATGAGAATGATATGATGCTTGTTGGAGACG

          *       2420         *       2440          *       2460
ATCCTTGGCAGGAGTTTTGTTGCATGGTTCGCAAAATCTTCATATACACGAAAGAGGAAG
ATCCTTGGCAGGAGTTTTGTTGCATGGTTCGTAAAATCTTCATATACACGAAAGAGGAGG

          *       2480         *       2500          *       2520
TGAGGAAGATGAACCCGGGGACTTTAAGCTGTAGGAGCGAGGAAGAAGCAGTTGTTGGGG
TGAGGAAGATGAACCCGGGAACTCTATGCTGTAGGAACGAGGAAGAACCAGTTGTTGGGG

          *       2540         *       2560          *       2580
AAGGATCAGATGCAAAGGACGCCAAGTCTGCATCAAATCCTTCATTGTCCAGCGCTGGCA
AAGGATCAGATGCAAAGGACGCGAAGTCTGCATCAAATCCTTCATTGTCCAGCGCCGGAA

ACTCTTAA
ACTCTTAA
```

Figure 9

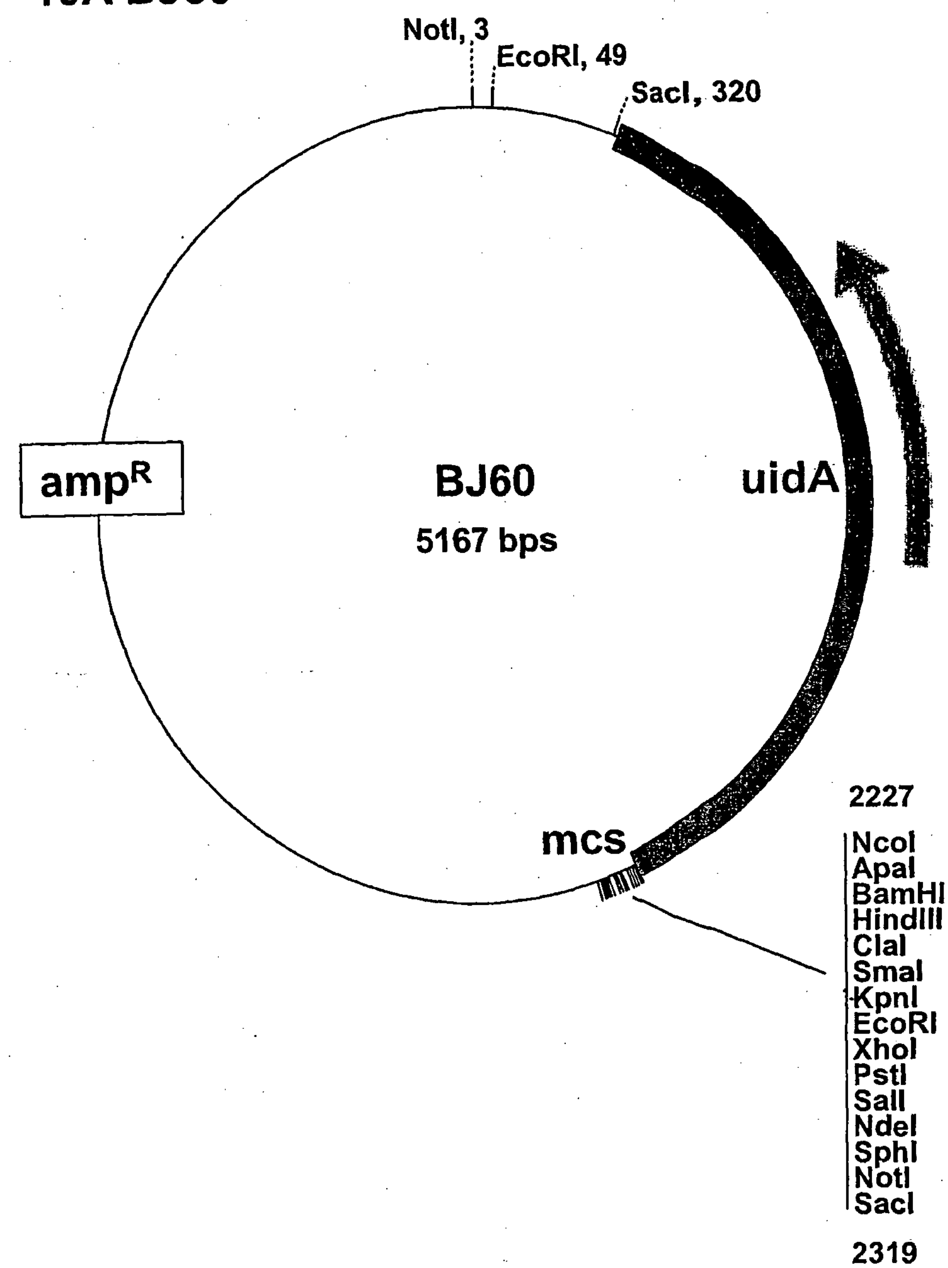
Alignment of MNT, BnARF2, OsARF2 proteins

```
                   *        20         *        40         *
MNTwt  : MASSEVSMKGNRG-GDNFSSSGFSDPKETRNVSVAGEGQKSNSTRSAAAERALDP
BnARF2 : MASSEVSMKGNRGRGENFSSAGYSDP------TVAGEAQKTQSNRSVAAERVVDP
OsARF2 : ----------------------------------------------------GDP

           60         *        80         *       100         *
MNTwt  : EAALYRELWHACAGPLVTVPRQDDRVFYFPQGHIEQVEASTNQAAEQQMPLYDLP
BnARF2 : EAALYRELWHACAGPLVTVPRQDDRVFYFPQGHIEQVEASTNQAAEQQMPLYDLP
OsARF2 : ---LYDELWHACAGPLVTVPRVGDLVFYFPQGHIEQVEASMNQVADSQMRLYDLP

                120         *       140         *       160
MNTwt  : SKLLCRVINVDLKAEADTDEVYAQITLLPEANQDENAIEKEAPLPPP--PRFQVH
BnARF2 : SKILCRVINVDLKAEADTDEVYAQITLLPEPVQDENSIEKEAPPPPP--PRFQVH
OsARF2 : SKLLCRVLNVELKAEQDTDEVYAQVMLMPEPEQNEMAVEKTTPTSGPVQARPPVR

             *       180         *       200         *       220
MNTwt  : SFCKTLTASDTSTHGGFSVLRRHADECLPPLDMSRQPPTQELVAKDLHANEWRFR
BnARF2 : SFCKTLTASDTSTHGGFSVLRRHADECLPPLDMSRQPPTQELVAKDLHASEWRFR
OsARF2 : SFCKTLTASDTSTHGGFSVLRRHADECLPPLDMTQSPPTQELVAKDLHSMDWRFR

                   *       240         *       260         *
MNTwt  : HIFRGQPRRHLLQSGWSVFVSSKRLVAGDAFIFLRGENGELRVGVRRAMRQQGNV
BnARF2 : HIFRGQPRRHLLQSGWSVFVSSKRLVAGDAFIFLRGENGELRVGVRRAMRQQGNV
OsARF2 : HIFRGQPRRHLLQSGWSVFVSSKRLVAGDAFIFLRGENGELRVGVRRAMRQLSNV

          280         *       300         *       320         *
MNTwt  : PSSVISSHSMHLGVLATAWHAISTGTMFTVYYKPRTSPSEFIVPFDQYMESVKNN
BnARF2 : PSSVISSHSMHLGVLATAWHAISTGTMFTVYYKPRTSPSEFIVPFDQYTESVKIN
OsARF2 : PSSVISSQSMHLGVLATAWHAINTKSMFTVYYKPRTSPSEFIIPYDQYMESVKNN

                340         *       360         *       380
MNTwt  : YSIGMRFKMRFEGEEAPEQRFTGTIVGIEESDPTRWPKSKWRSLKVRWDETSSIP
BnARF2 : YSIGMRFKMRFEGEEAPEQRFTGTIVGIEDSDPTRWAKSKWRSLKVRWDETTSIP
OsARF2 : YSVGMRFRMRFEGEEAPEQRFTGTIIGSENLDPV-WPESSWRSLKVRWDEPSTIP

             *       400         *       420         *       440
MNTwt  : RPDRVSPWKVEPALAPPALSPVPMPRPKRPRSNIAPSSPDSSMLTREGTTKANMD
BnARF2 : RPDRVSPWKIEPALSPPALSPVPMPRPKRPRSNLASSTPDSSMRIREGSSKANMD
OsARF2 : RPDRVSPWKIEPASSPP-VNPLPLSRVKRPRPNAPPASPESPILTKEAAIKVDTD
```

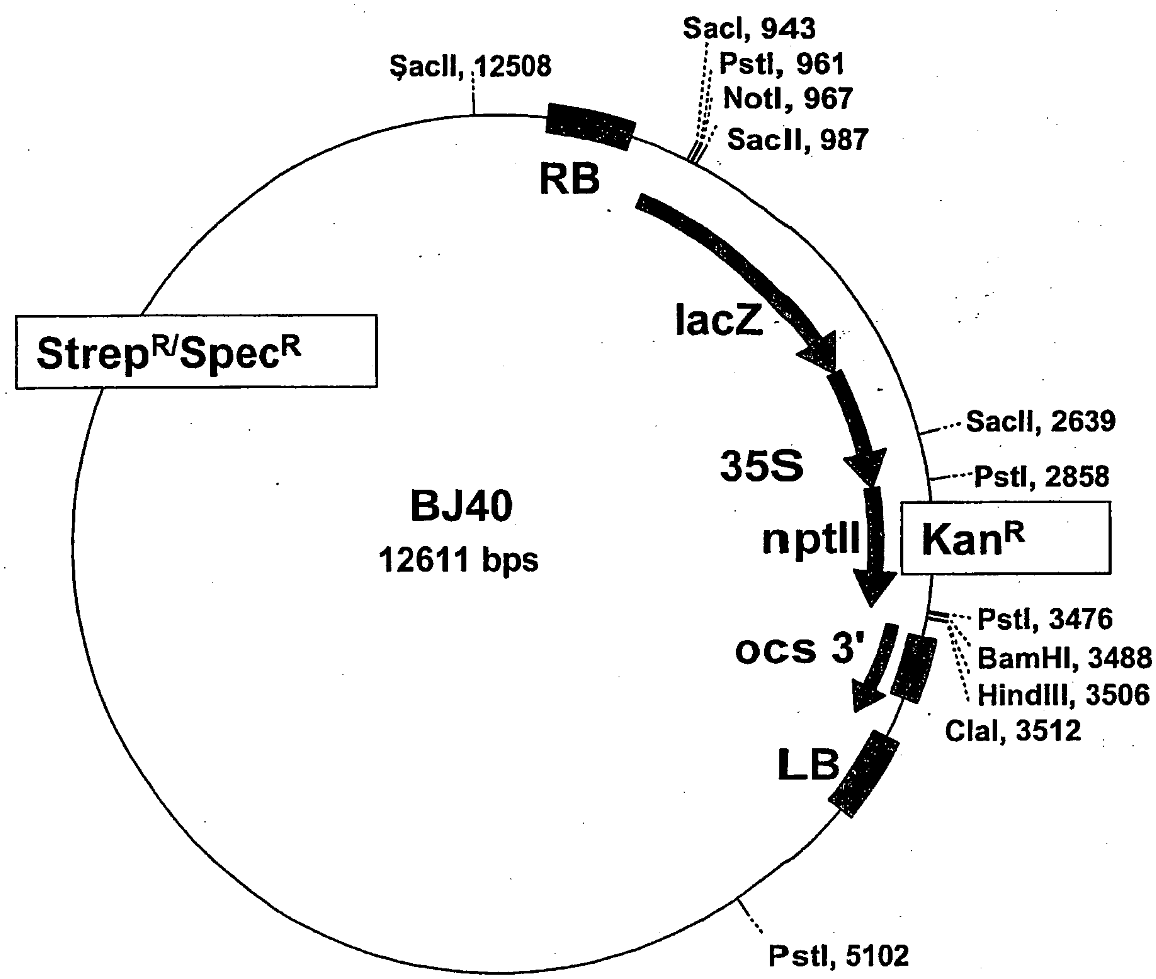
```
                  *        460        *        480        *
MNTwt  : PLPA--SGLSRVLQGQEYSTLRTKHTESVECDAPENS-VVWQSSADDDKVDVVSG
BnARF2 : PLPA--SGLSRVLQGQEYPTLRTKHVESVECDAPENS-VVWQSSTDDDKVDVISA
OsARF2 : PAQAQRSQNSTVLQGQEQMTLRSNLTESNDSDVTAHKPMMWSPSPNAAKAHPLTF

           500        *        520        *        540        *
MNTwt  : SRRYGSENWMSSARHEPTYTDLLSGFGTNIDPSHGQRIPFYDH-SSSPSMPA-KR
BnARF2 : SRRY--ENWISSGRHGPTCTDLLSGFGTNIEPPHGHQIPFYDRLSSPPSVAA-RK
OsARF2 : QQRPPMDNWMQLGRRETDFKDVRSG-SQSFGDSPGFFMQNFDE--APNRLTSFKN

                560        *        580        *        600
MNTwt  : ILSDSEGKFDYLANQWQMIHSGLSLKLHESPKVPAATDASLQGRCNVKYSEYPVL
BnARF2 : ILSDQDGKFEYLANQW-MMHSGLSLKLHESPKVPAASDASFQGIGNPNYGEYALP
OsARF2 : QFQDQ-GSARHFSDPYYYV----------SPQPSLTVESSTQMHTDSK--ELHFW

           *        620        *        640        *        660
MNTwt  : NGLSTENAGGNWPIRPRALNYYEEVVNAQAQAQAR-EQ--VTKQPFTIQE-ETAK
BnARF2 : RAVTTENAAGNWPIRPRALNYFEEAVHAQ-----AR-EH--VTKRPAVVQE-EAAK
OsARF2 : NGQST--VYGNSRDRPQNFRFEQNSSSWLNQSFARPEQPRVIRPHASTAPVELEK

                  *        680        *        700        *
MNTwt  : SREGNCRLFGIPL-TNNM--NGTDSTMSQRNN--LNDAAGLTQIASPKVQDLSDQ
BnARF2 : PRDGNCRLFGIPL-VNNV--NGTDTTLSQRNN--LNDPAGPTQMASPKVQDLSDQ
OsARF2 : TEGSGFKIFGFKVDTTNAPNNHLSSPMAATHEPMLQTPSSLNQLQPVQTDCIPEV

           720        *        740        *        760        *
MNTwt  : SKGSKSTNDHREQGRPFQTNNPHPKDAQTKTN--SSRSCTKVHKQGIALGRSVDL
BnARF2 : SKGSKSTNDHREQGRPFPVSKPHPKDVQTKTN--SCRSCTKVQKQGIALGRSVDL
OsARF2 : SVSTAGLATENEKSG--QQAQQSSKDVQSKTQVASTRSCTKVHKQGVALGRSVDL

                780        *        800        *        820
MNTwt  : SKFQNYEELVAELDRLFEFNGELMAPKKDWLIVYTDEENDMMLVGDDPWQEFCCM
BnARF2 : SKFQNYEELVTELDRLFEFNGELMAPKKDWLIVYTDDENDMMLVGDDPWQEFCCM
OsARF2 : SKFSNYDELKAELDKMFEFDGELVSSNKNWQIVYTDNEGDMMLVGDDPWEEFCSI

           *        840        *        860        *
MNTwt  : VRKIFIYTKEEVRKMNPGTLSCRSEEEAVFGEGSDAKDAKSASNPSLSSAGNS
BnARF2 : VRKIFIYTKEEVRKMNPGTLCCRNEEEPVFGEGSDAKDAKSASNPSLSSAGNS
OsARF2 : VRKIYIYTKEEVQKMNSKSNAPRKD---------DSSENEKGHLPMPNKSDN-
```

Figure 10
Vectors used for cloning

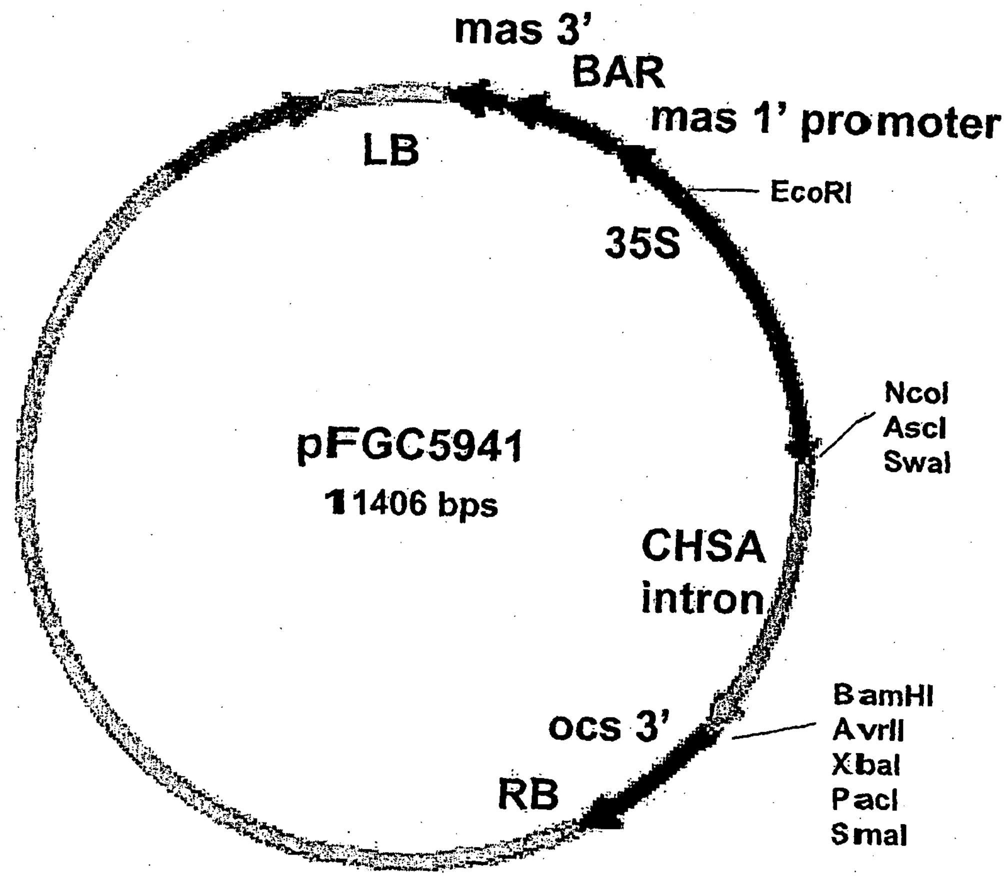
10A BJ60



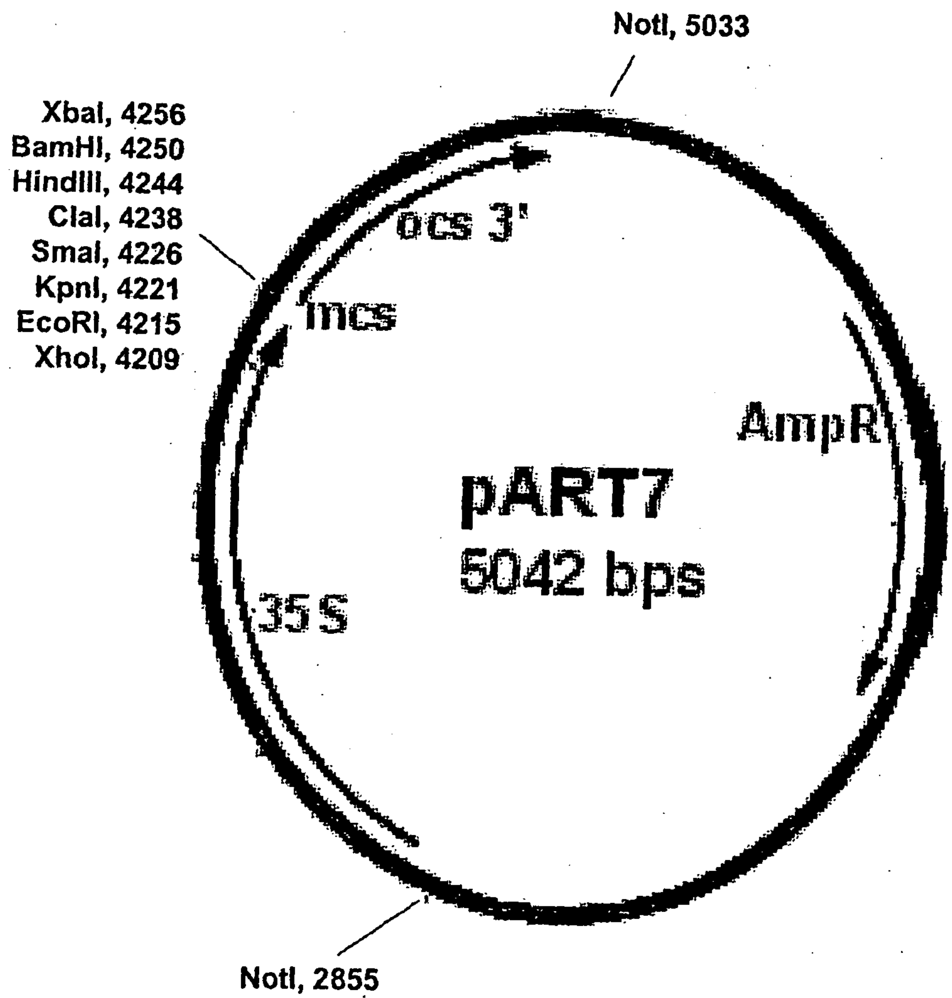
10B BJ40


SacI, 943
PstI, 961
NotI, 967
SacII, 987
SacII, 12508
RB
lacZ
Strep^R/Spec^R
SacII, 2639
35S
PstI, 2858
BJ40
12611 bps
nptII
Kan^R
PstI, 3476
ocs 3'
BamHI, 3488
HindIII, 3506
ClaI, 3512
LB
PstI, 5102

10C pFGC5941



10D pART7


NotI, 5033
XbaI, 4256
BamHI, 4250
HindIII, 4244
ClaI, 4238
SmaI, 4226
KpnI, 4221
EcoRI, 4215
XhoI, 4209
ocs 3'
mcs
AmpR
pART7
5042 bps
35 S
NotI, 2855

0E BJ36

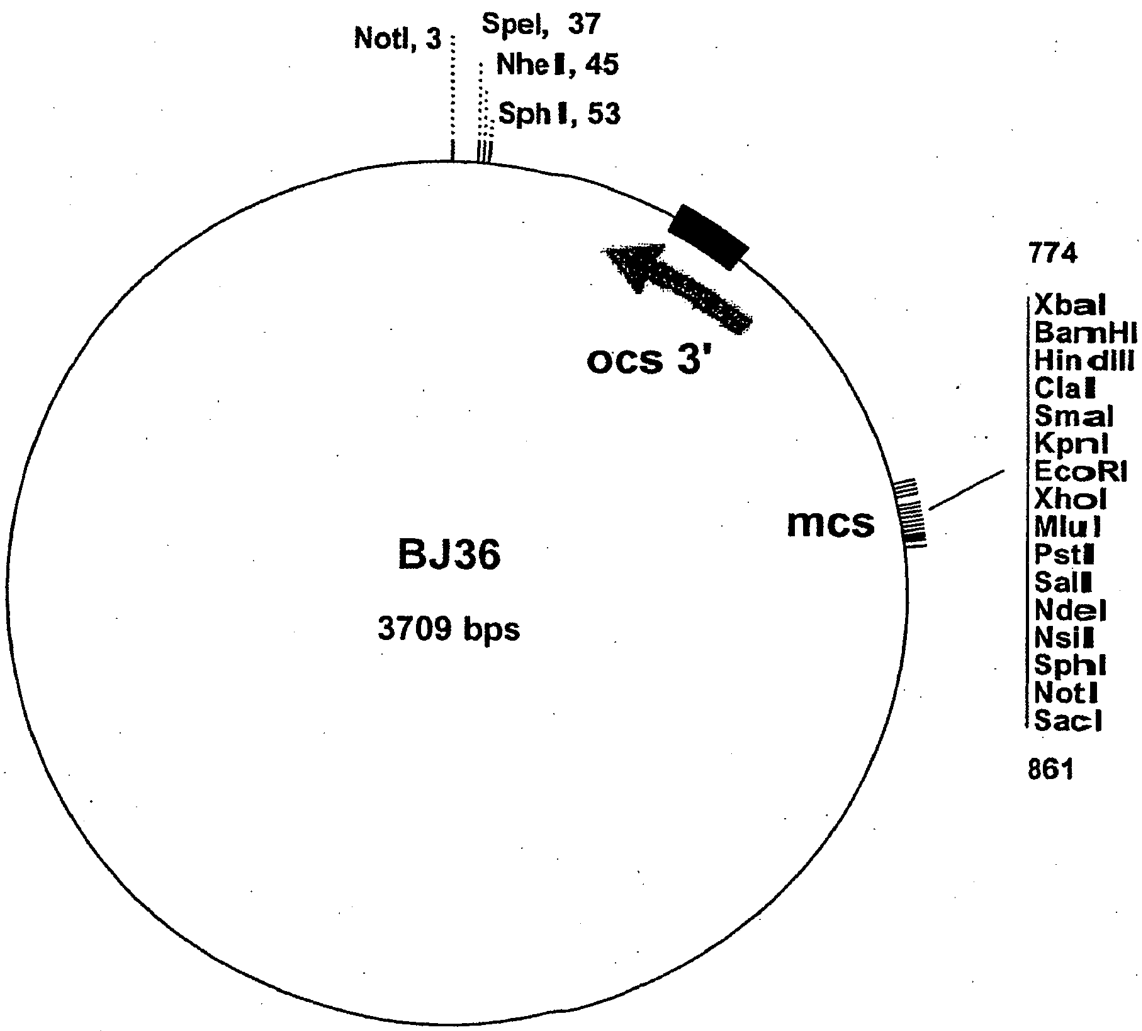
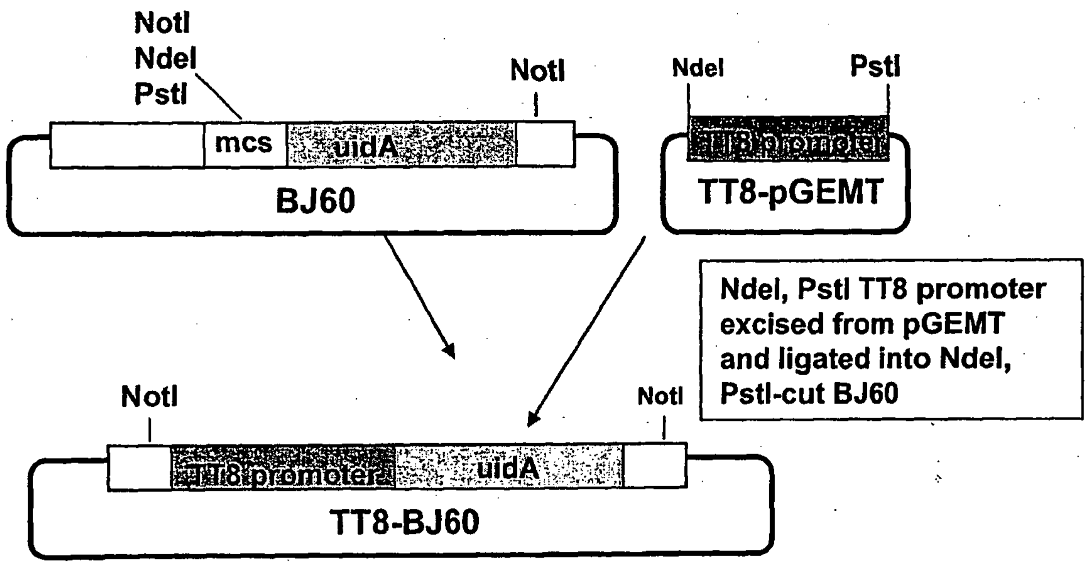

NotI, 3
SpeI, 37
NheI, 45
SphI, 53
ocs 3'
774
XbaI
BamHI
HindIII
ClaI
SmaI
KpnI
EcoRI
XhoI
MluI
PstI
SalI
NdeI
NsiI
SphI
NotI
SacI
861
mcs
BJ36
3709 bps

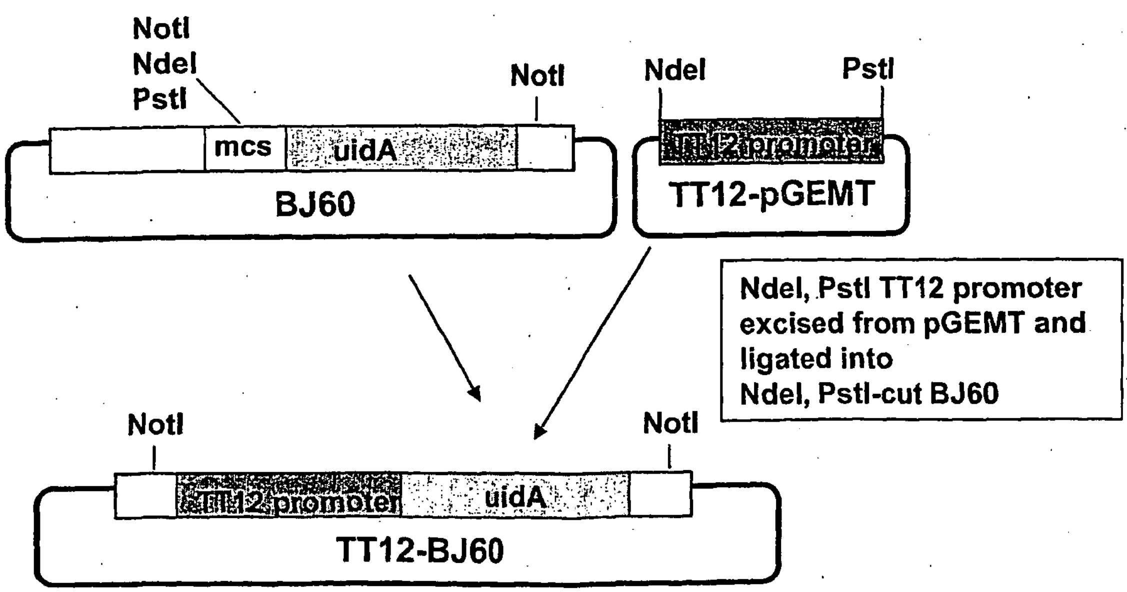
Figure 11

Cloning strategy, Example 3

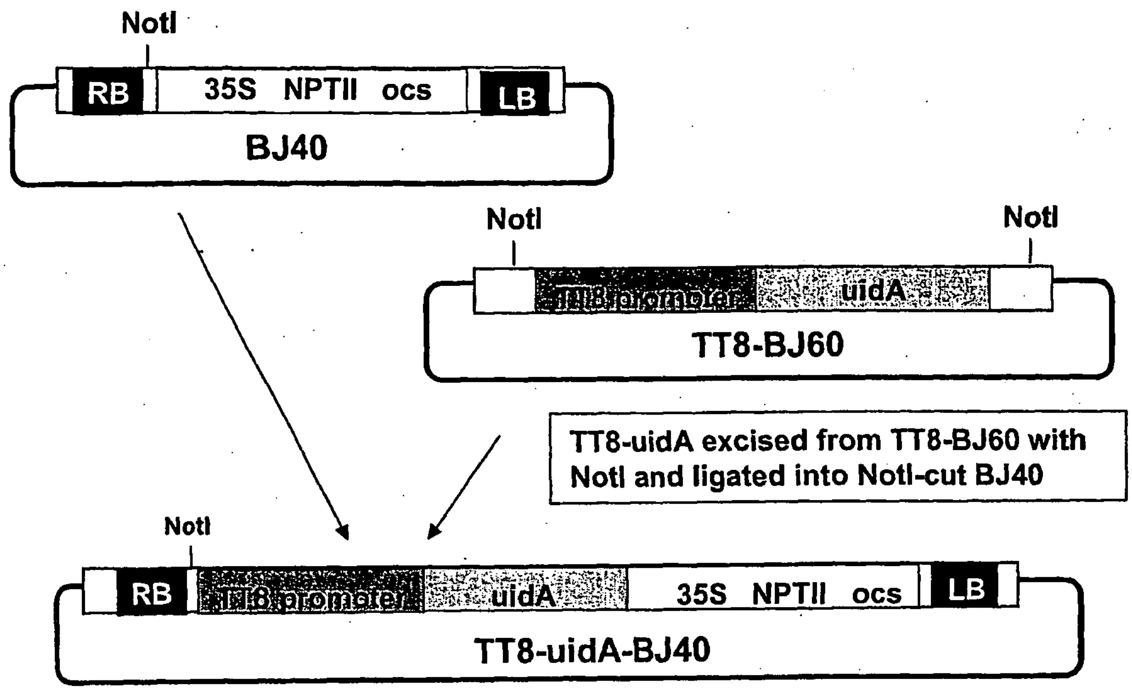
Example 3a(i)



Example 3a(ii)



Example 3b(i)



Example 3b(ii)

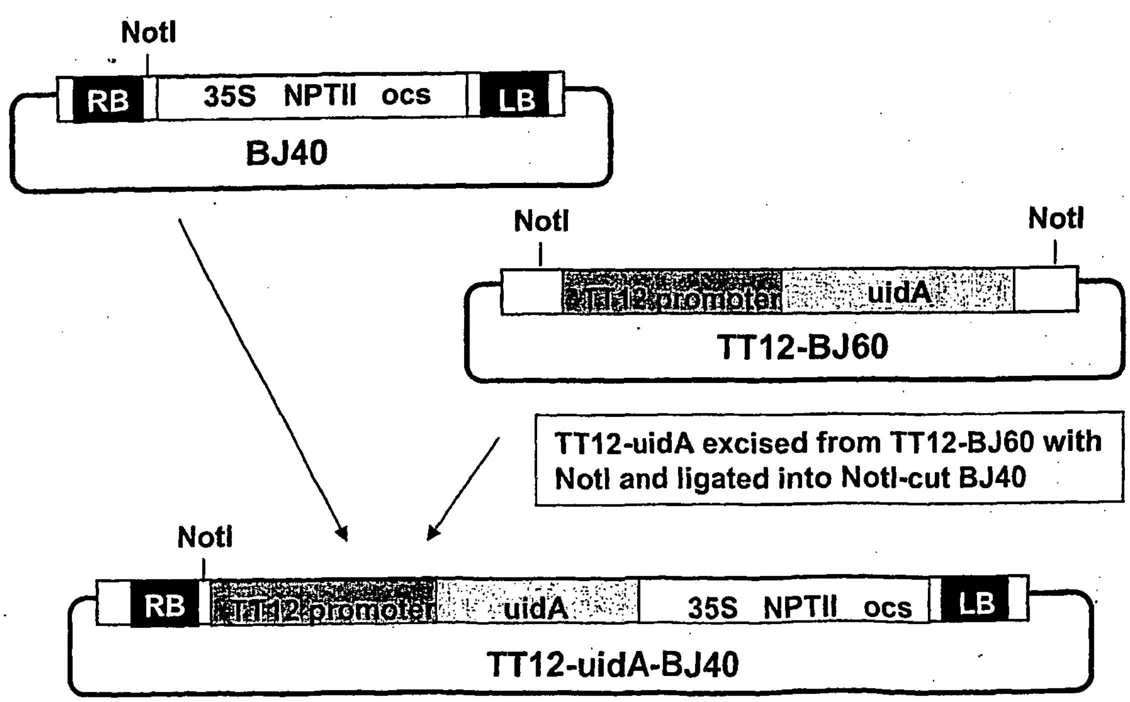


Figure12

TT12::uidA

Figure 13A
Cloning strategy, Example 4

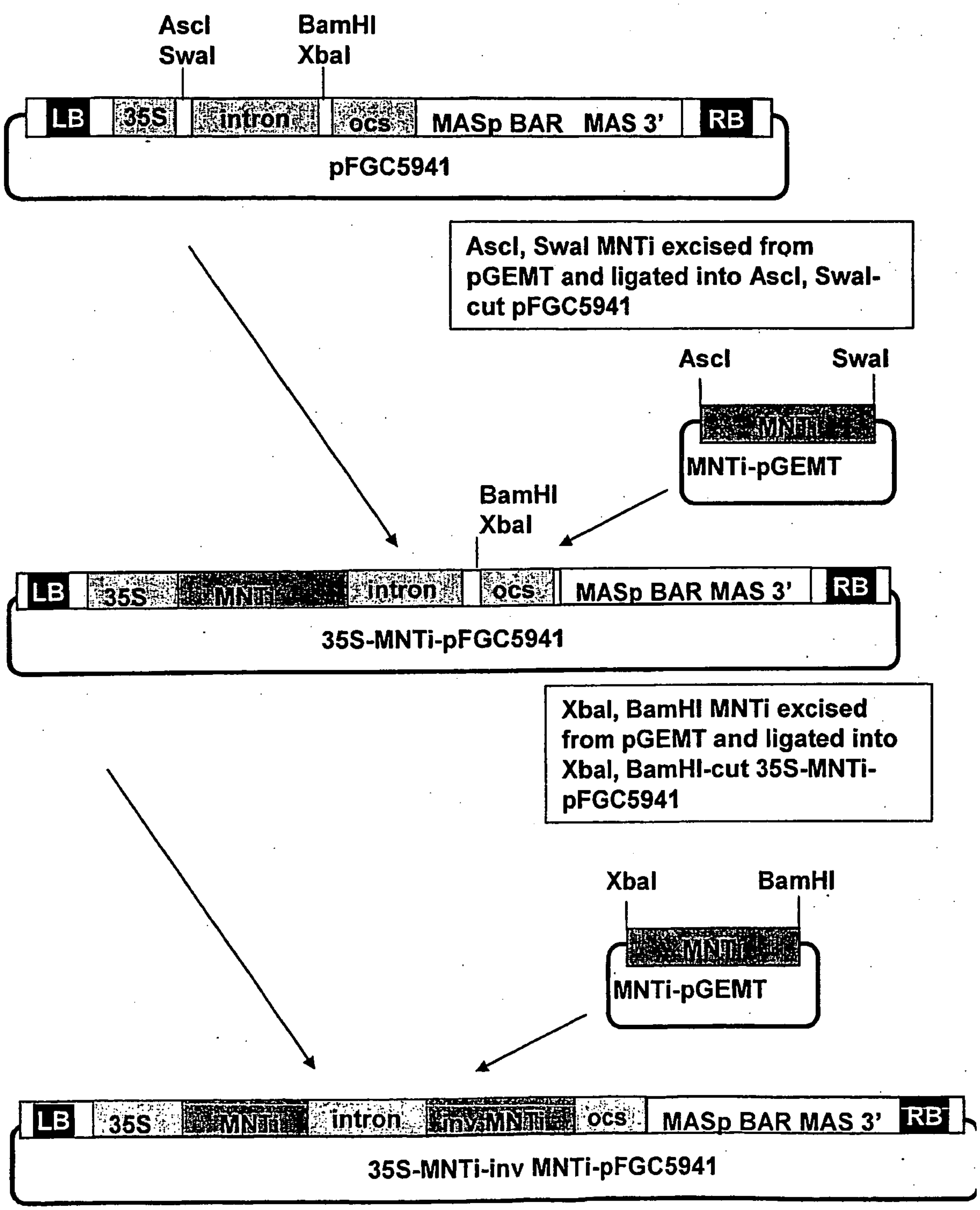


Figure 13B

Plants transformed with the *35S::MNT* RNAi vector

Example 4

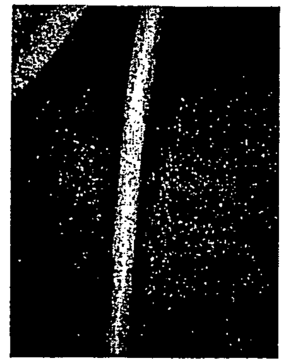
Primary inflorescence

wild-type Col-3

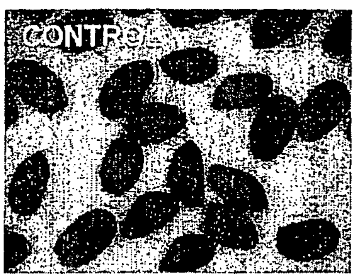
***35S::MNT* RNAi line 3**

Primary inflorescence stem

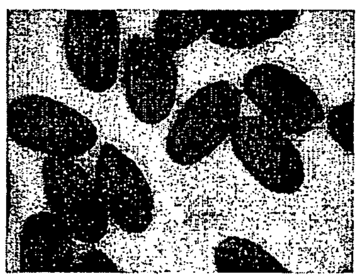
wild-type Col-3



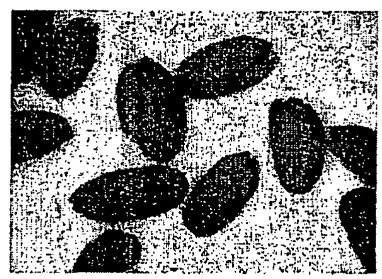
***35S::MNT* RNAi line 3**



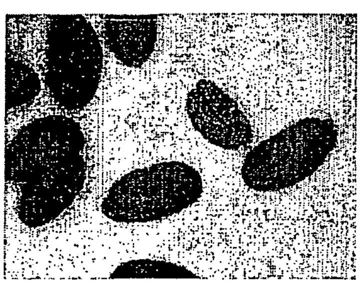
wild-type Col-3
mean wt 13.8 μg



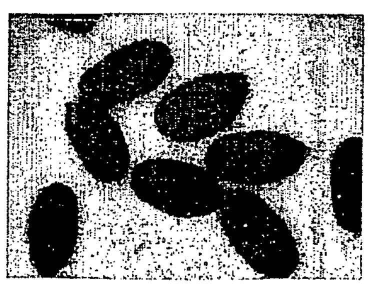
***35S::MNT* RNAi line 1**
mean wt 34.0 μg



***35S::MNT* RNAi line 2**
mean wt 35.6 μg



***35S::MNT* RNAi line 3**
mean wt 34.8 μg



***35S::MNT* RNAi line 4**
mean wt 36.7 μg

Figure 14
Cloning strategy, Example 5

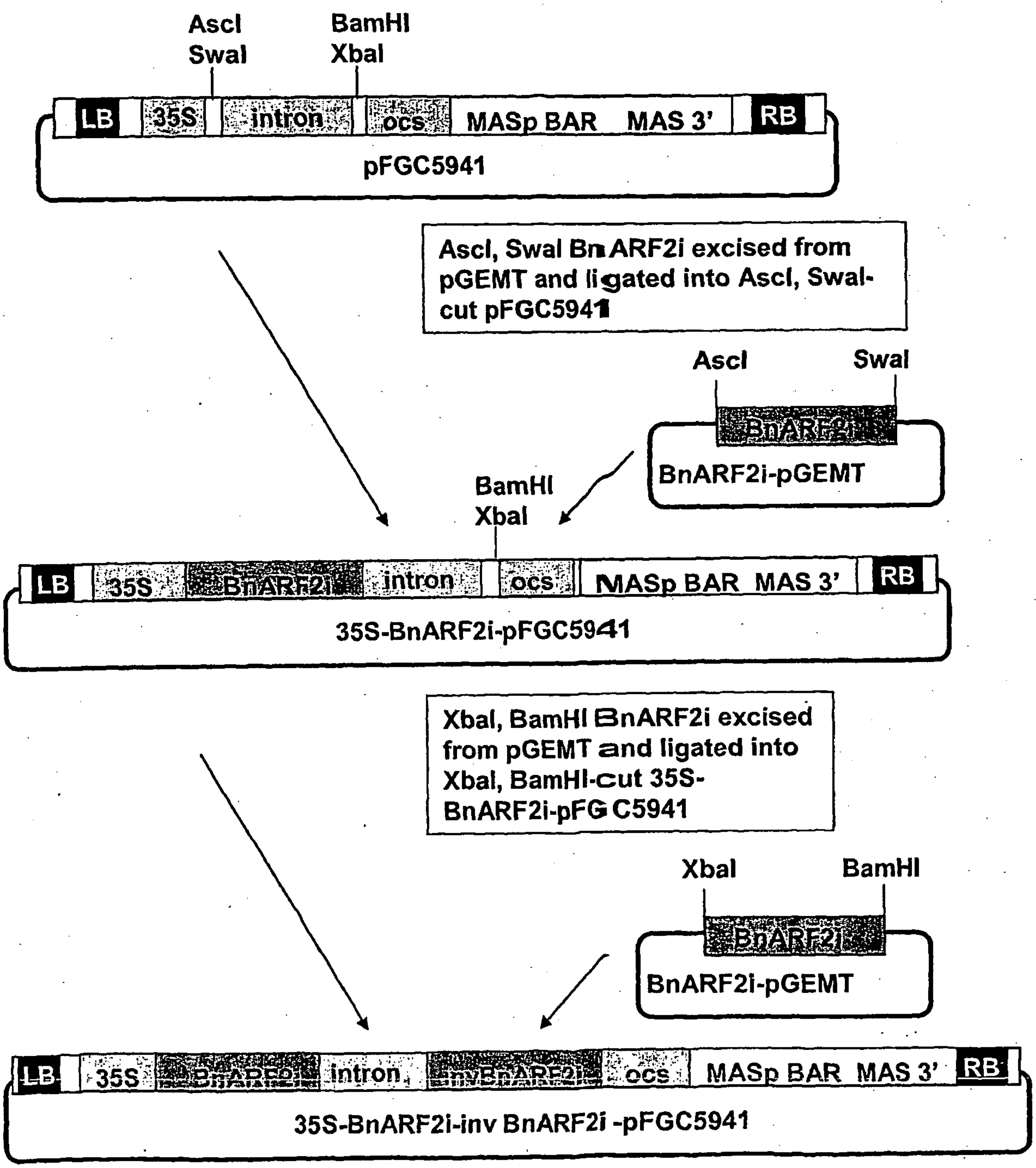
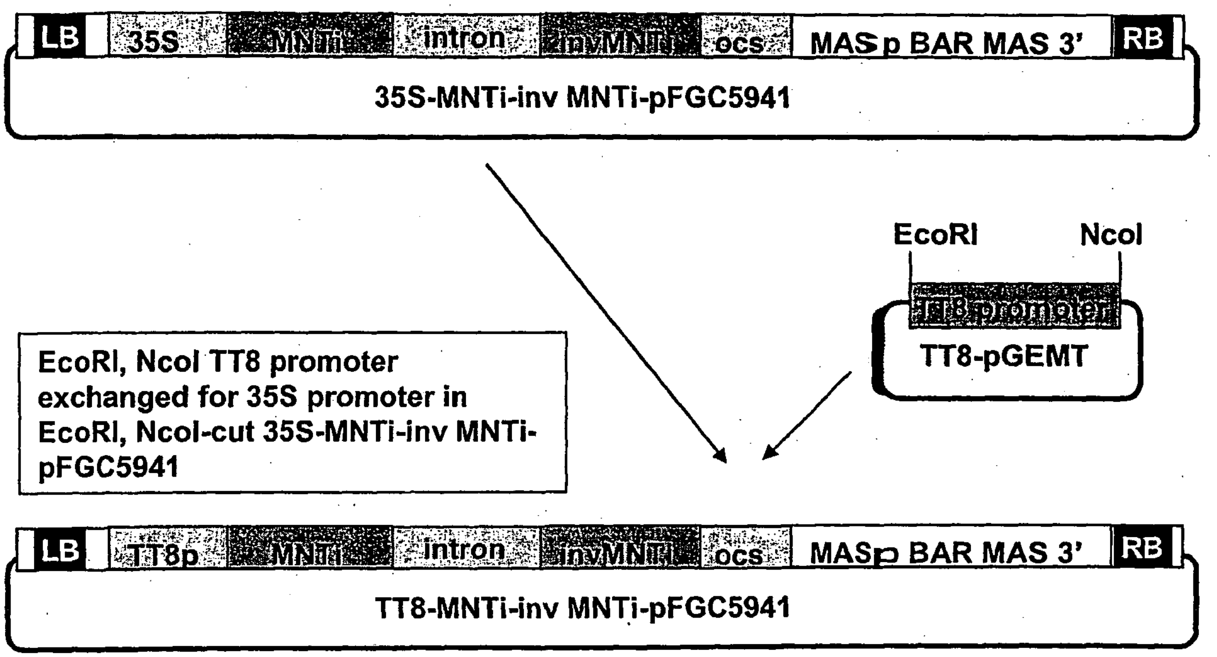


Figure 15

Cloning strategy, Example 6

Example 6a(i)



Example 6a(ii)

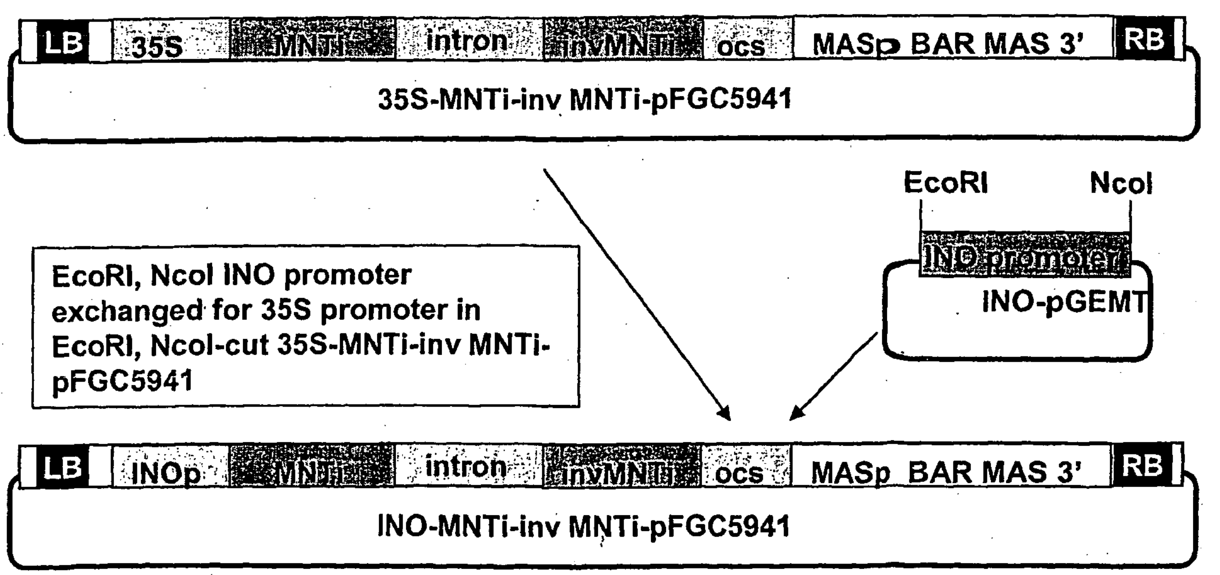
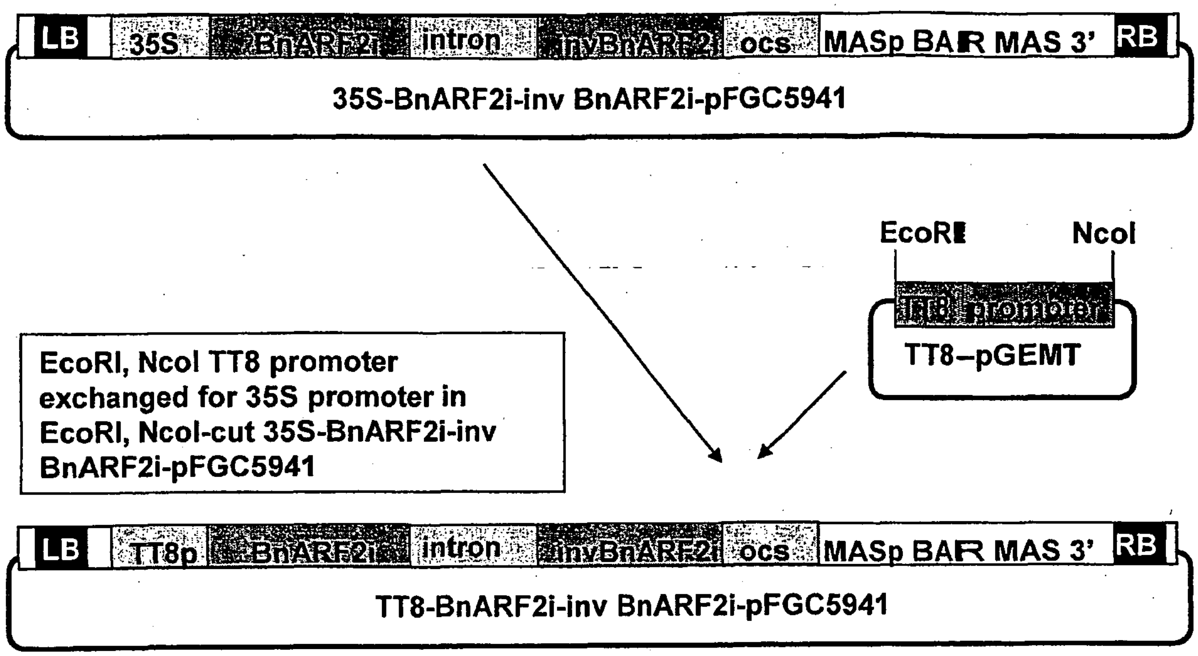


Figure 16
Cloning strategy, Example 7

Example 7a(i)



Example 7a(ii)

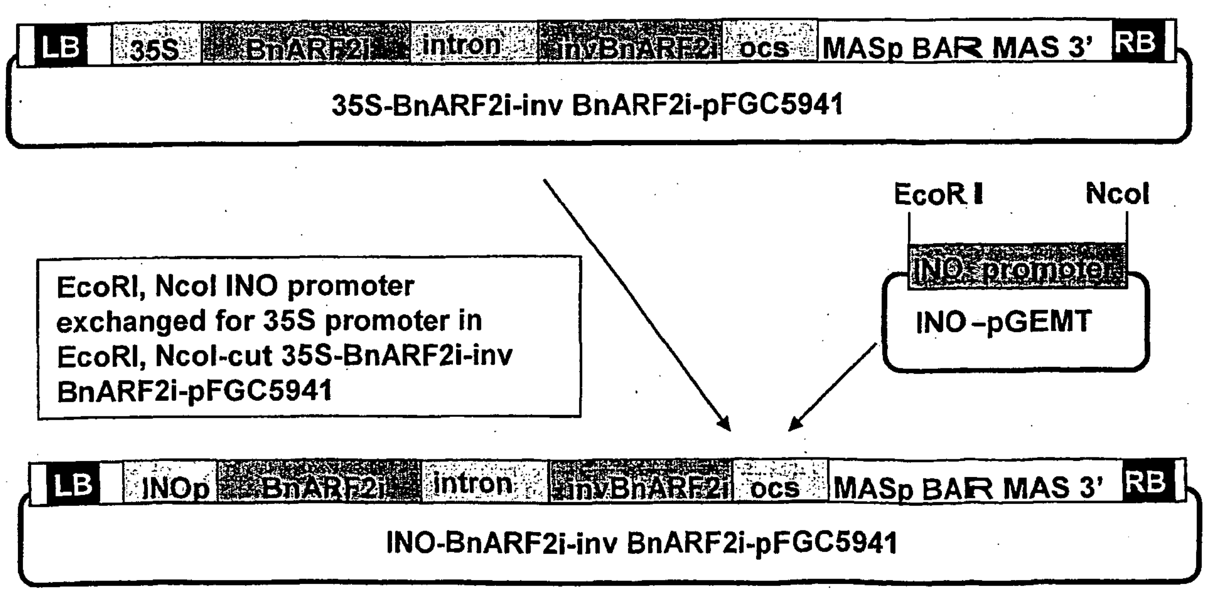
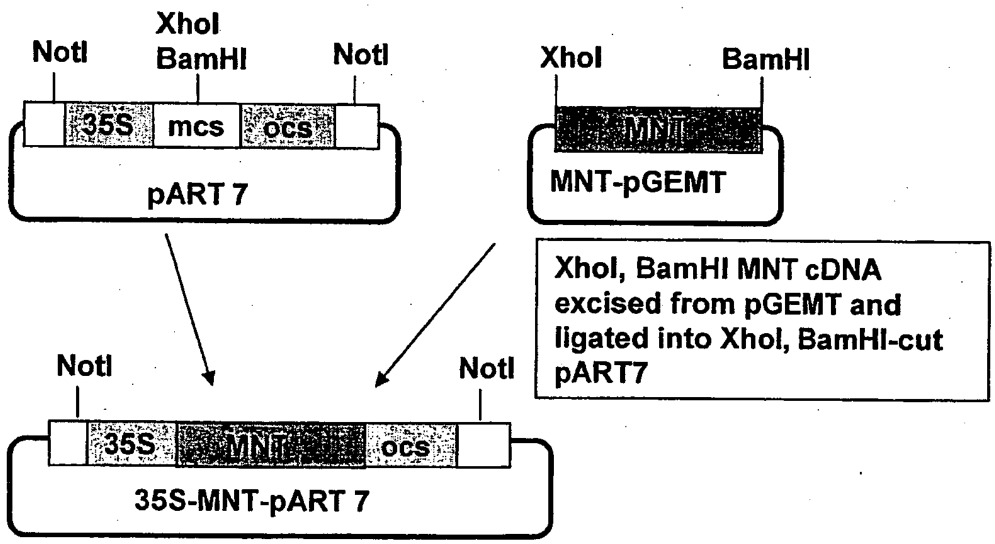
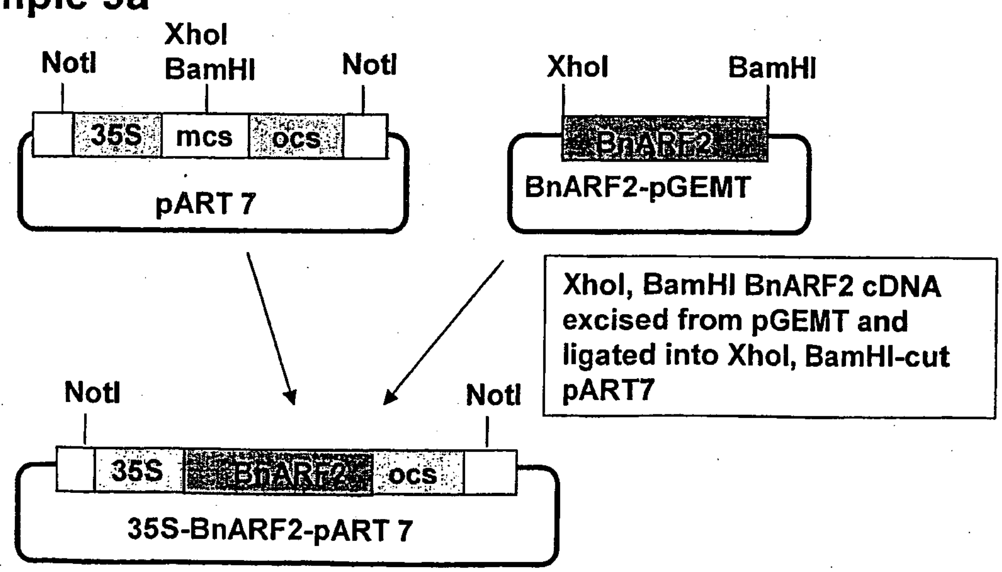


Figure 17A
Cloning strategy, Examples 8, 9

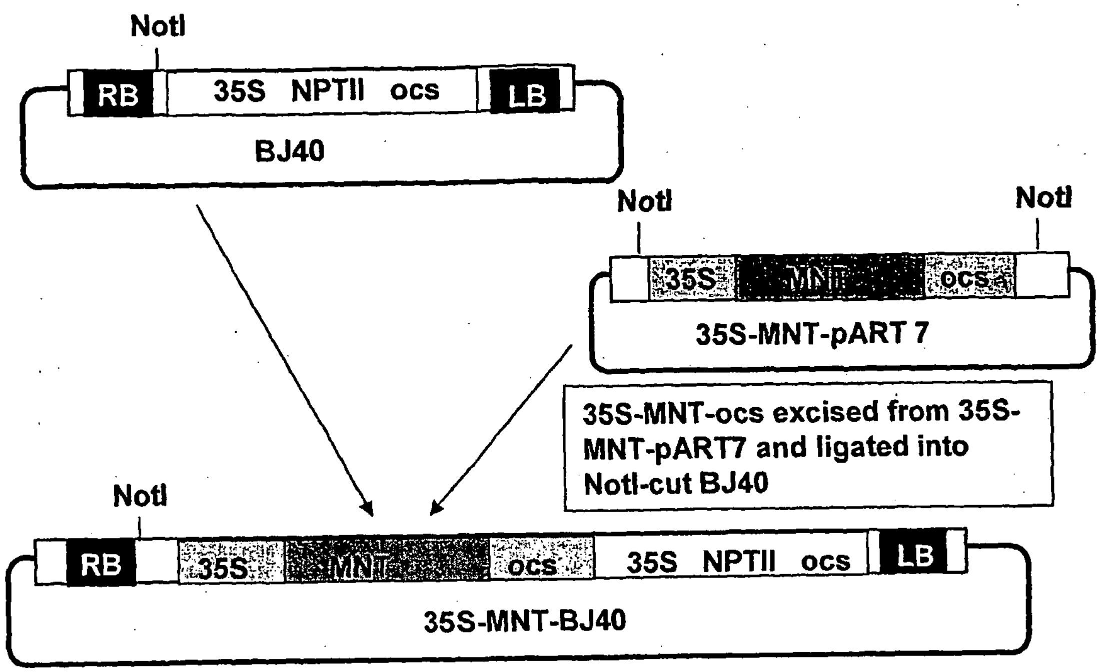
Example 8a



Example 9a



Example 8b



Example 9b

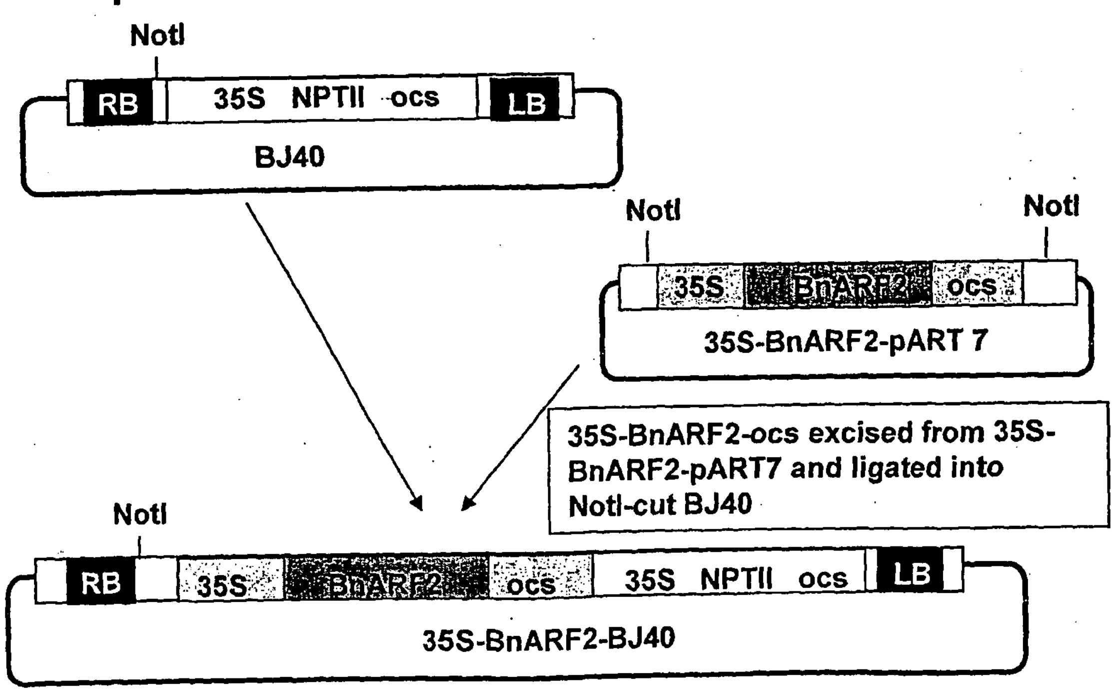
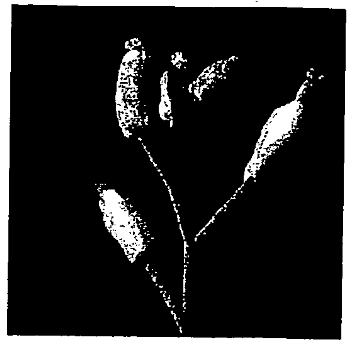


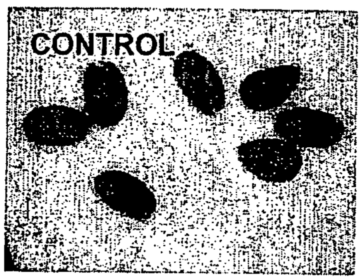
Figure 17B

Analysis of wild-type plants transformed with the *35S::MNT* vector

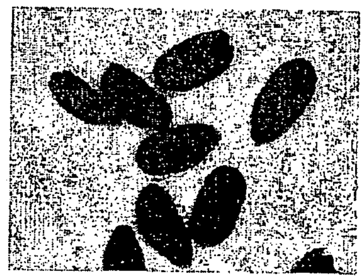
Example 8

35S::MNT

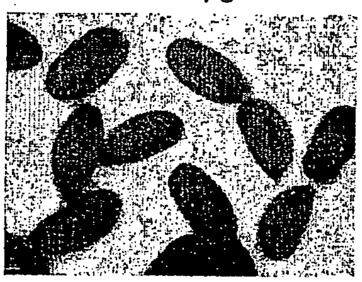




wild-type Col-3
mean wt 15.0 µg



***35S::MNT* line 1**
mean wt 23.1 µg

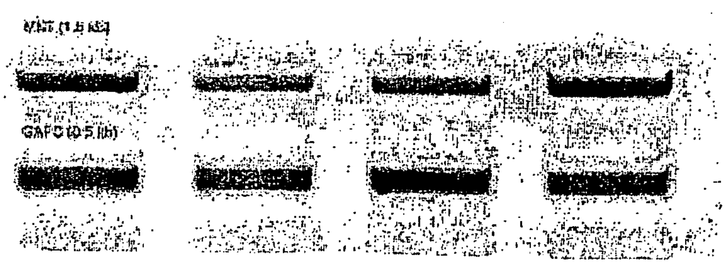


***35S::MNT* line 2**
mean wt 28.7 µg

***35S::MNT* line 3**
mean wt 24.6 µg

Semiquantitative RT-PCR

w.t. 35S::MNT line 1 line 2 line 3



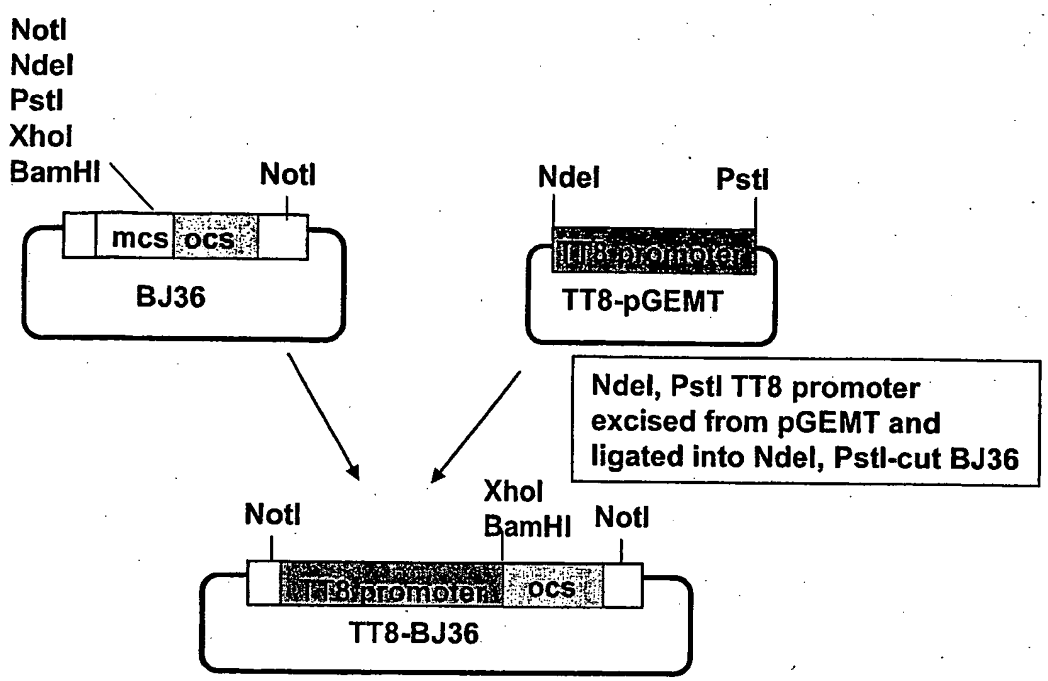
MNT cDNA (1.5 kb)

GAPC cDNA (0.5 kb)

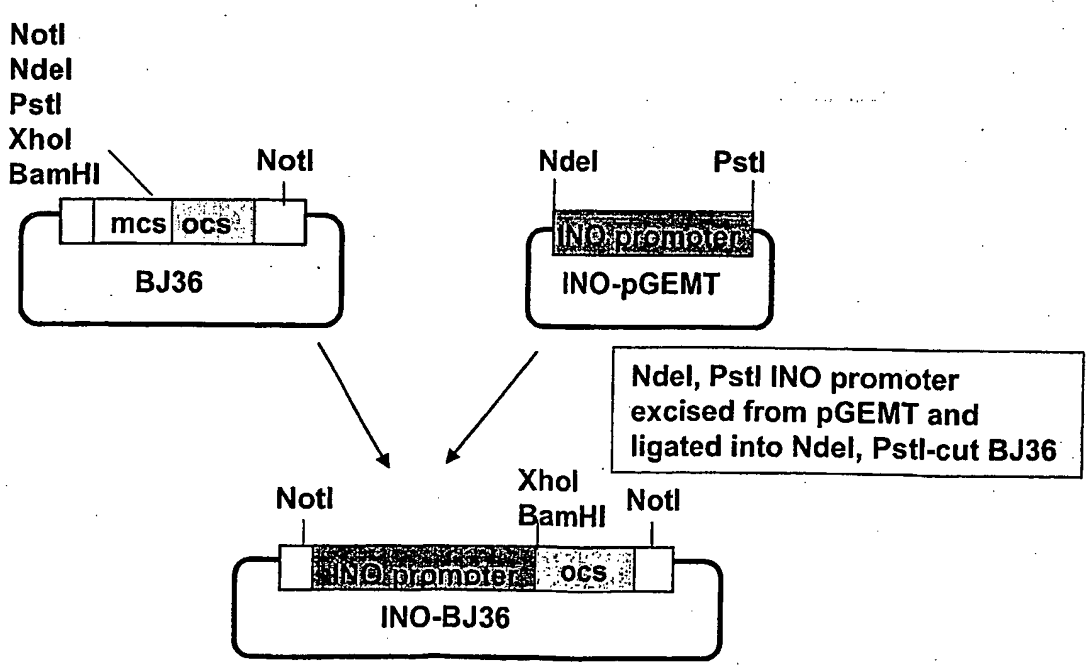
Figure 18

Cloning strategy, Example 10

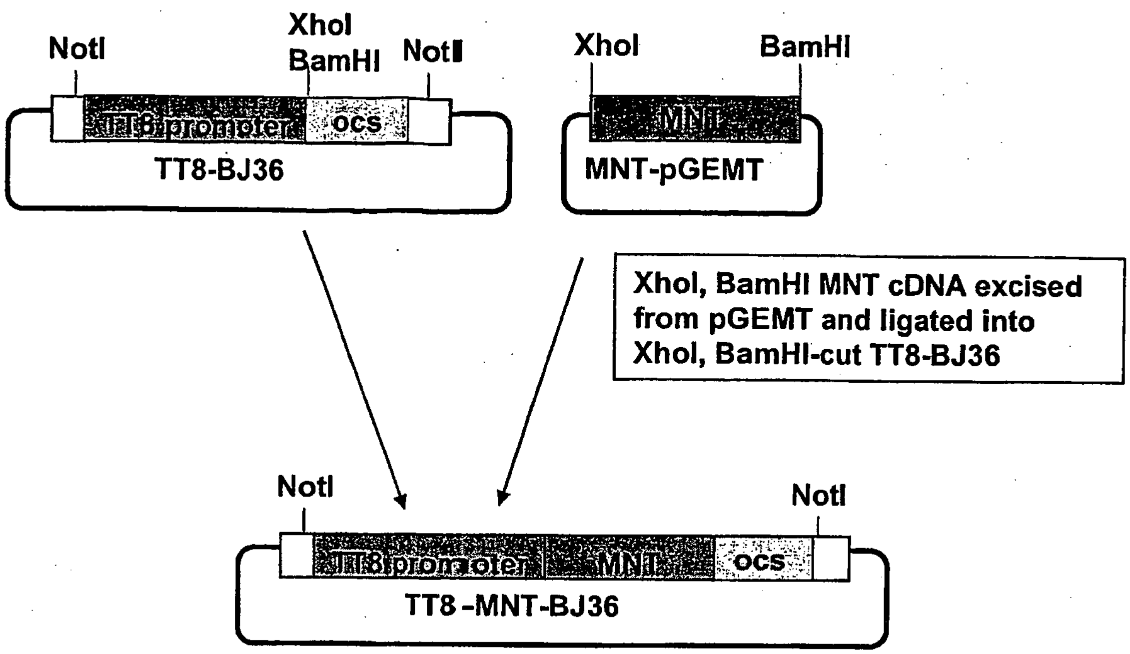
Example 10a(i)



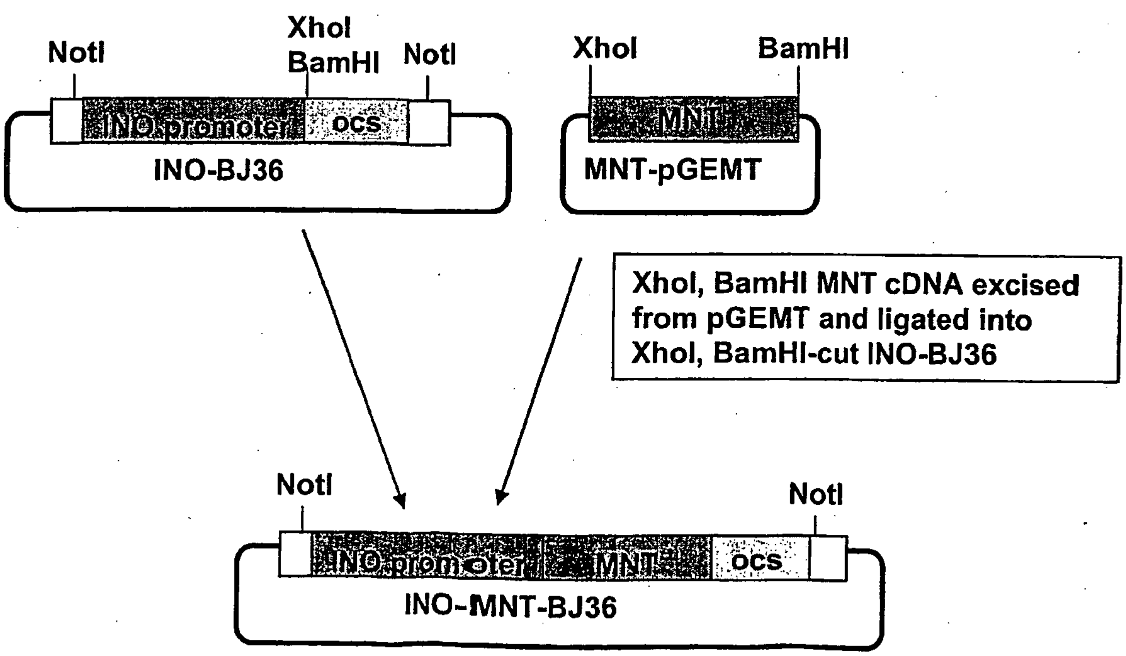
Example 10a(ii)



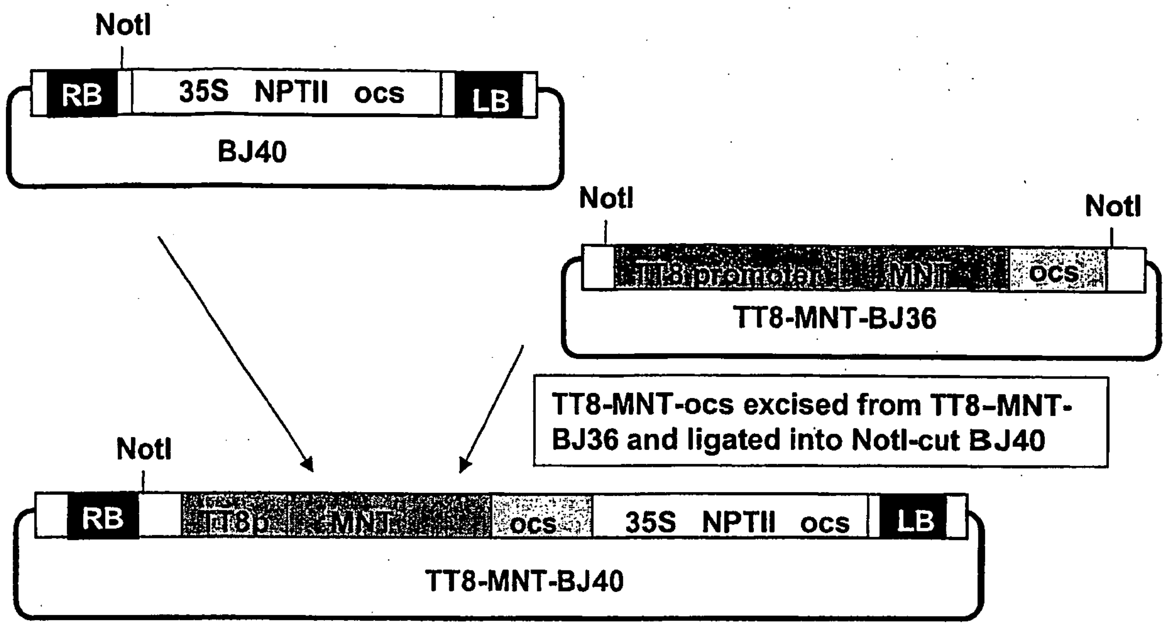
Example 10b(i)



Example 10b(ii)



Example 10c(i)



Example 10c(ii)

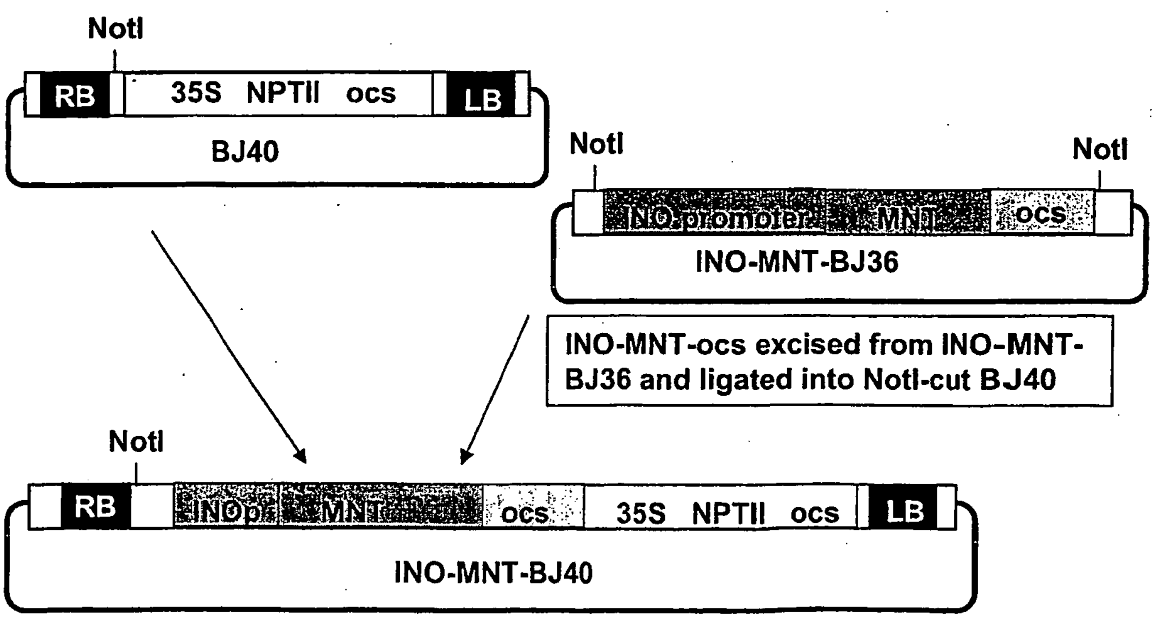
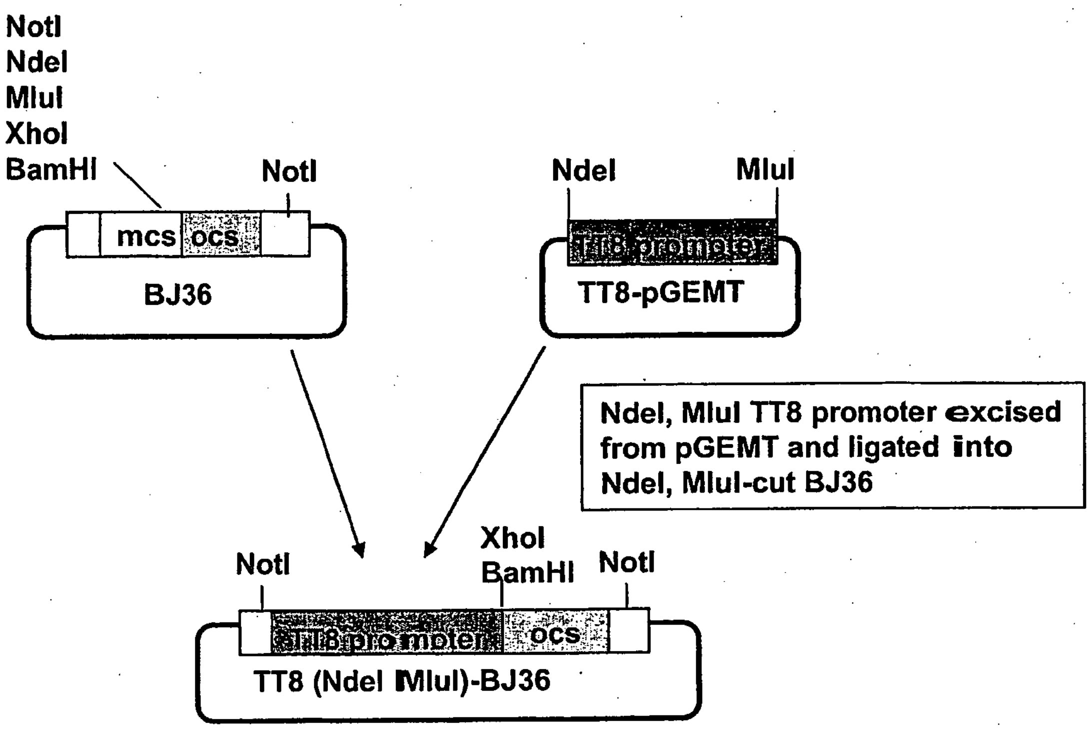


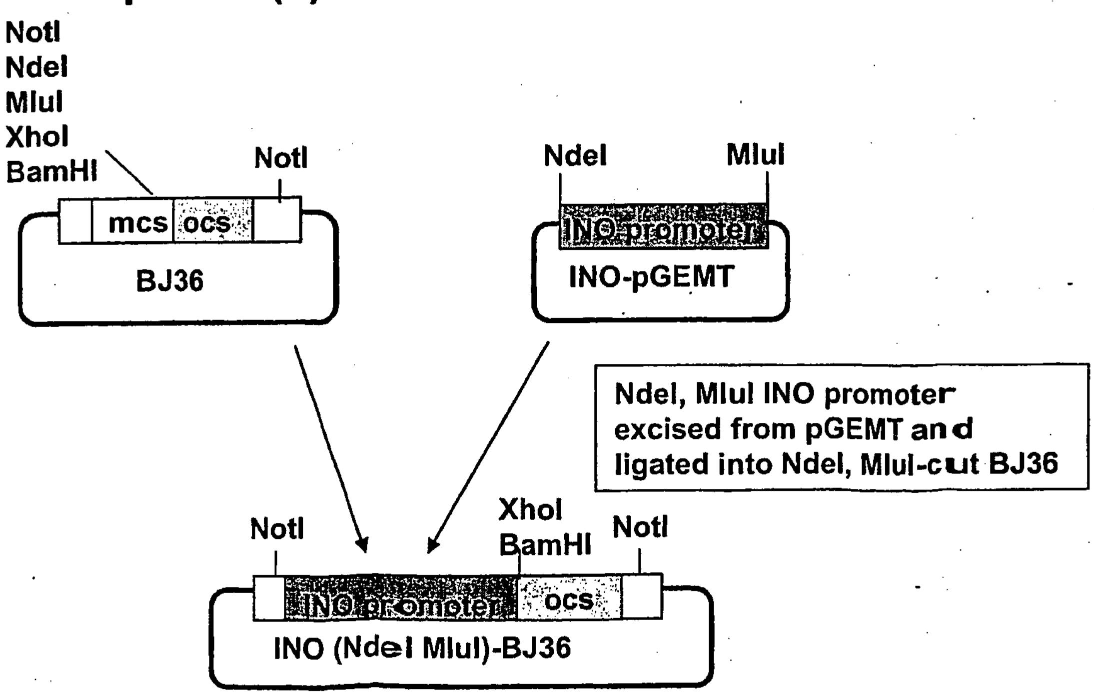
Figure 19

Cloning strategy, Example 11

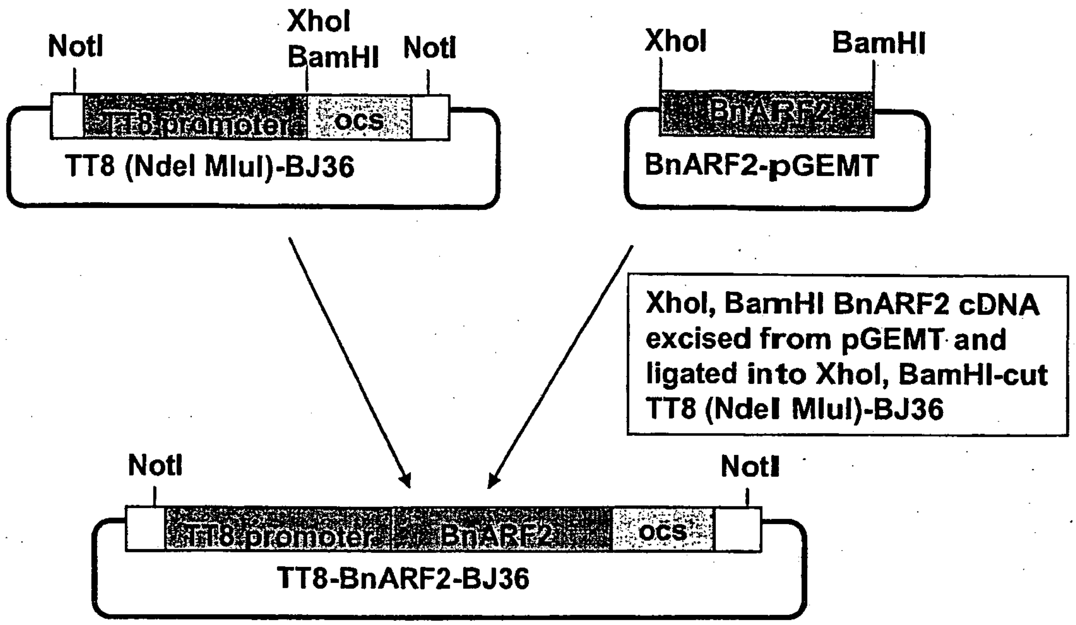
Example 11a(i)



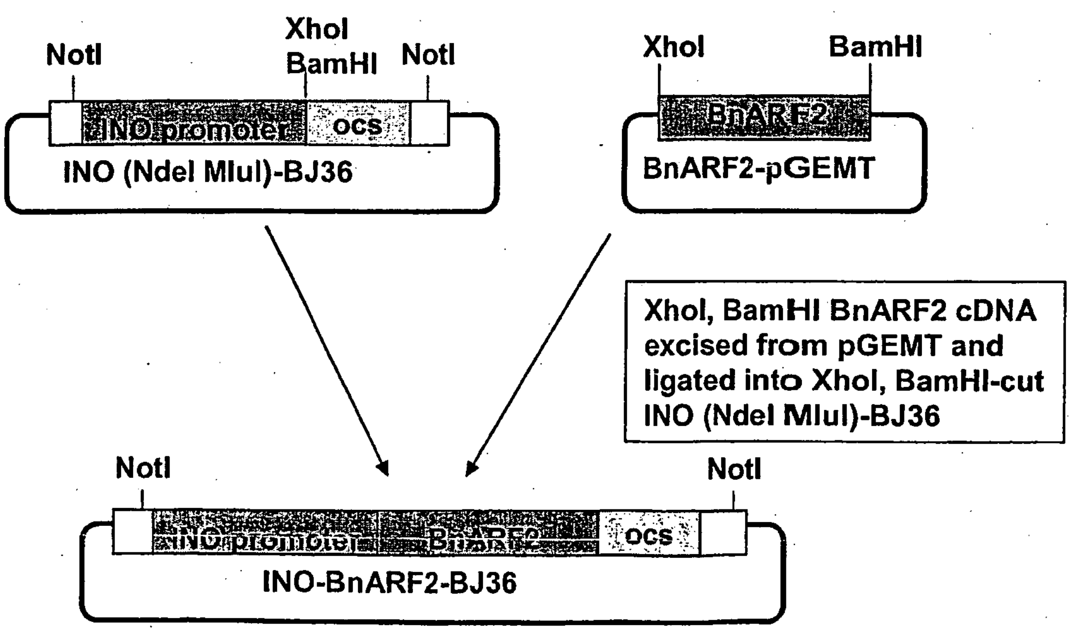
Example 11a(ii)



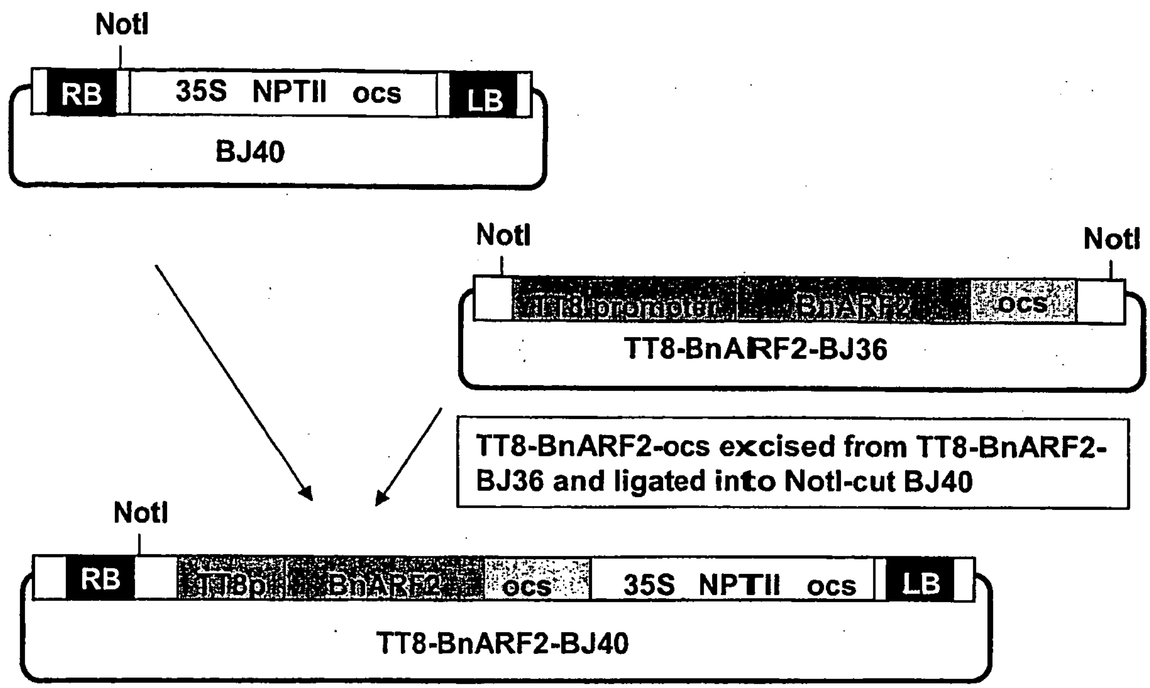
Example 11b(i)



Example 11b(ii)



Example 11c(i)



Example 11c(ii)

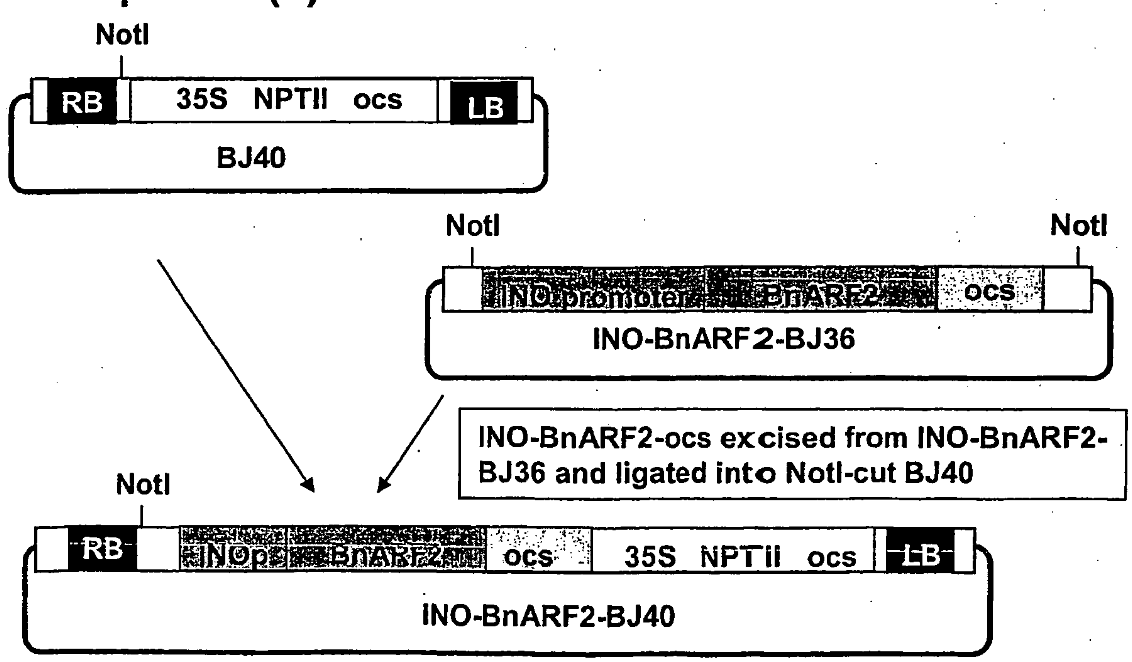
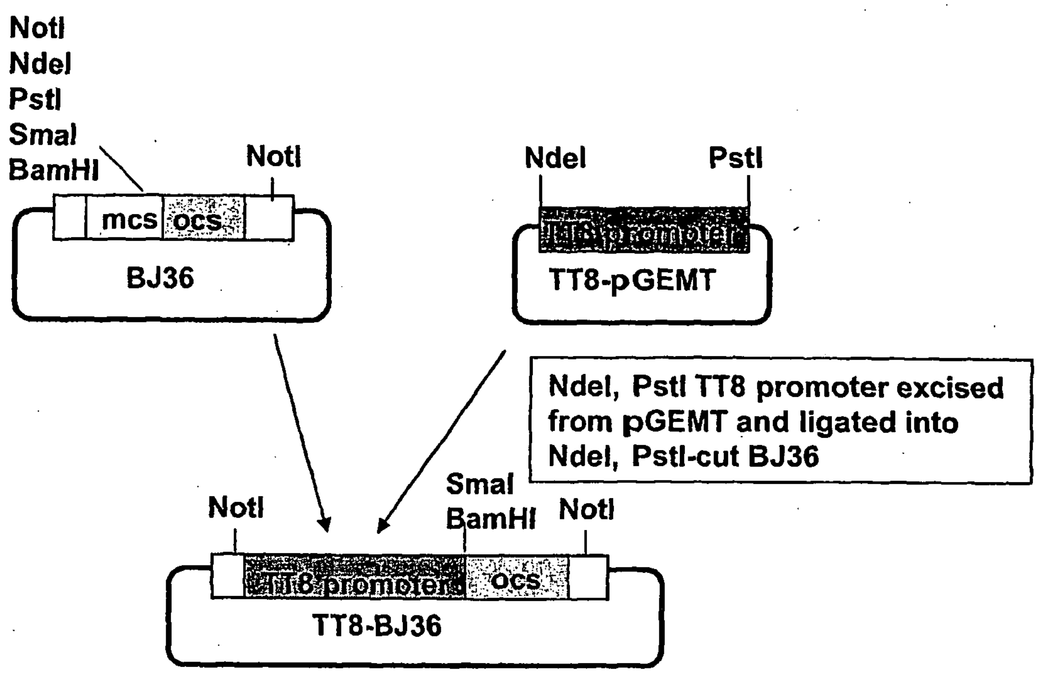


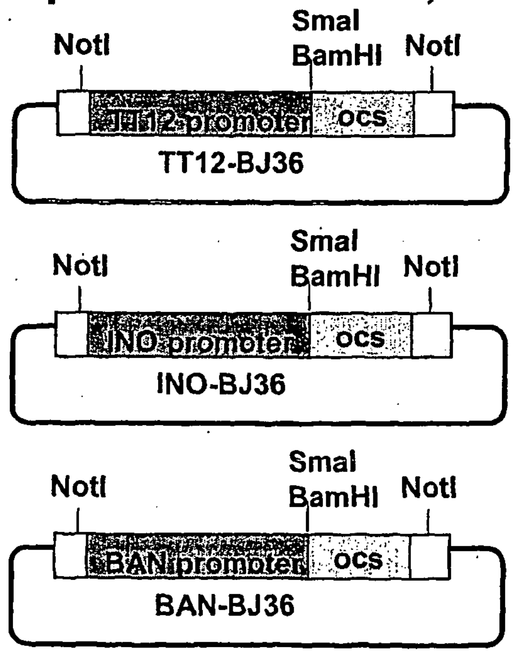
Figure 20

Cloning strategy, Examples 12, 13

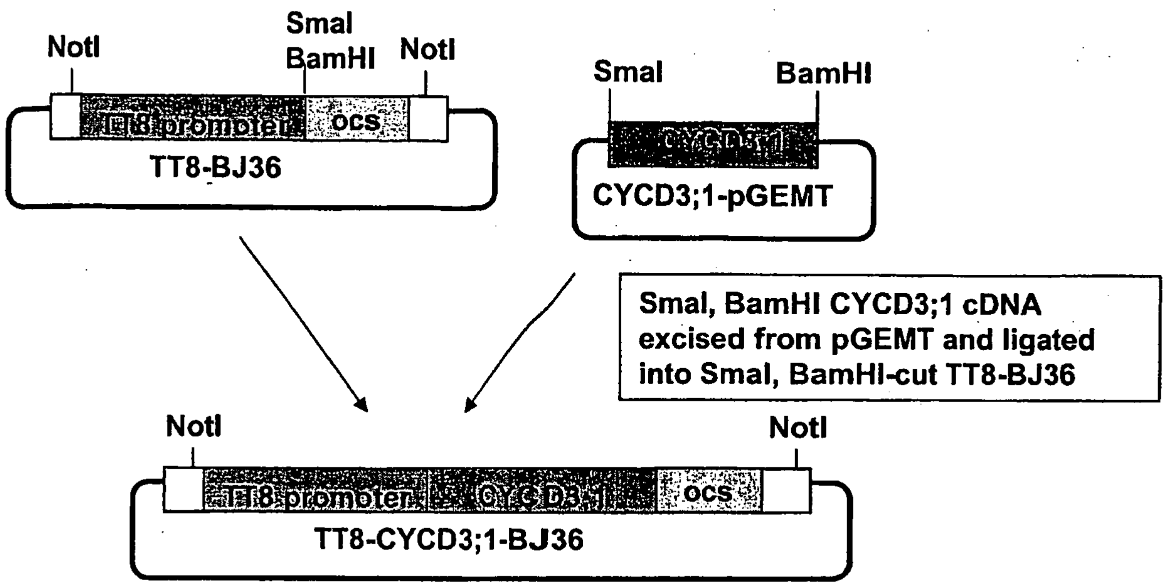
Examples 12a, 13a



Repeat process with TT12, INO, BAN promoters



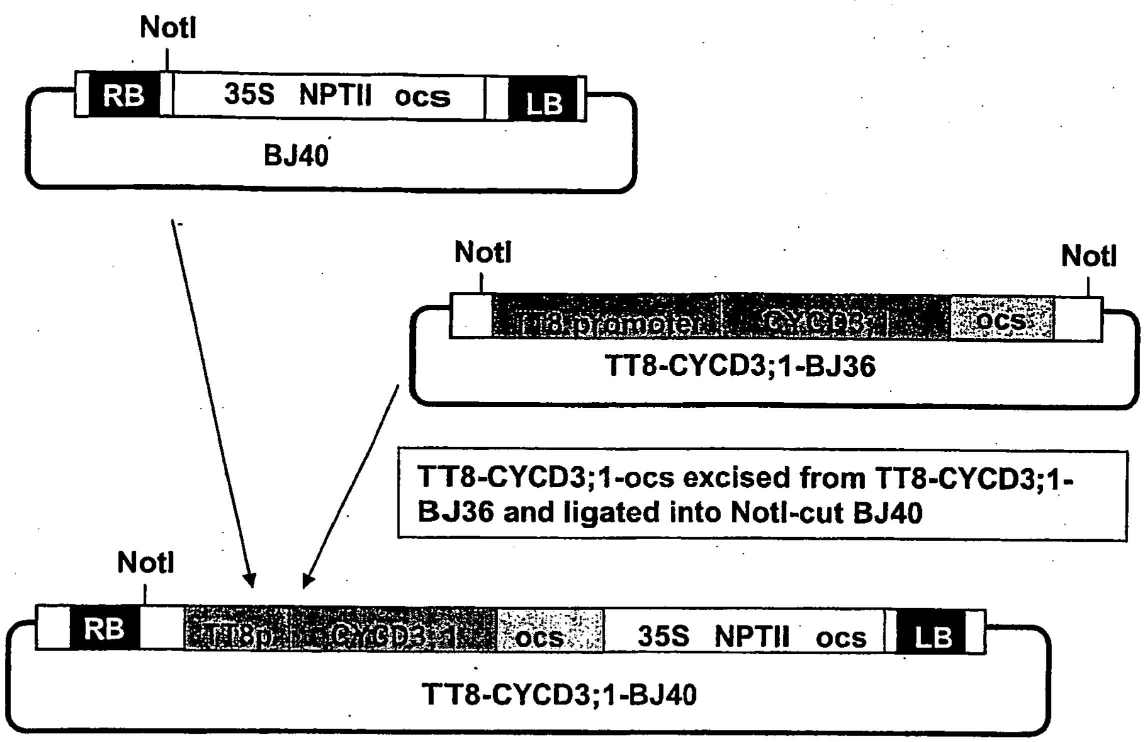
Examples 12b, 13b



Repeat process with IPT1, ANT, CYCB1;1 cDNAs and TT12, INO, BAN promoters

TT8-IPT1-BJ40	INO-CYCD3;1-BJ40
TT8-ANT-BJ40	INO-IPT1-BJ40
TT8-CYCB1;1-BJ40	INO-ANT-BJ40
TT12-CYCD3;1-BJ40	INO-CYCB1;1-BJ40
TT12-IPT1-BJ40	BAN-CYCD3;1-BJ40
TT12-ANT-BJ40	BAN-IPT1-BJ40
TT12-CYCB1;1-BJ40	BAN-ANT-BJ40
	BAN-CYCB1;1-BJ40

Example 12c, 13c



Repeat process with all BJ36 constructs shown in Example 12b

TT8-IPT1-BJ40

TT8-ANT-BJ40

TT8-CYCB1;1-BJ40

TT12-CYCD3;1-BJ40

TT12-IPT1-BJ40

TT12-ANT-BJ40

TT12-CYCB1;1-BJ40

INO-CYCD3;1-BJ40

INO-IPT1-BJ40

INO-ANT-BJ40

INO-CYCB1;1-BJ40

BAN-CYCD3;1-BJ40

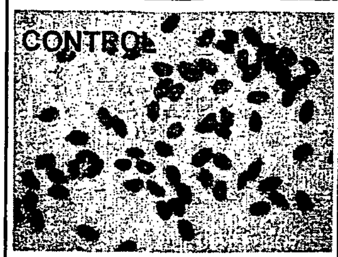
BAN-IPT1-BJ40

BAN-ANT-BJ40

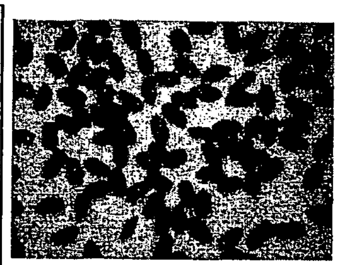
BAN-CYCB1;1-BJ40

Figure 21A

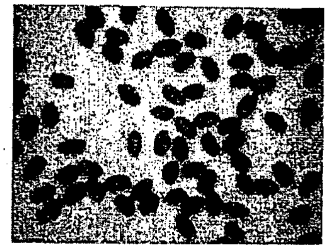
Expression cassettes to increase seed size



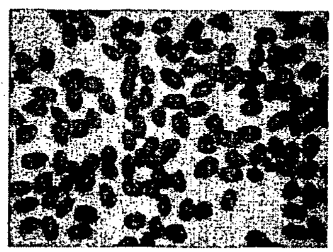
TT8::uidA line 12
mean wt 15.1 µg



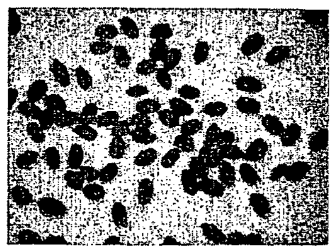
TT8::CYCD3;1 line 11
mean wt 29.2 µg



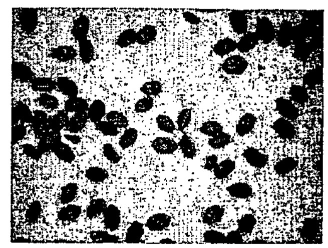
TT8::CYCD3;1 line 18
mean wt 28.1 µg



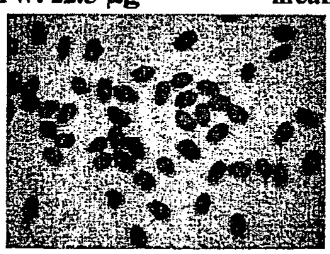
TT8::CYCD3;1 line 19
mean wt 22.5 µg



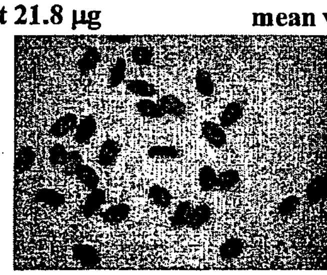
TT8::IPT1 line 38
mean wt 21.8 µg



TT8::IPT1 line 28
mean wt 23.4 µg



TT8::IPT1 line 32
mean wt 20.8 µg



TT8::IPT1 line 40
mean wt 30.6 µg

Distribution of seed weights in TT8::uidA (control), TT8::CYCD3;1, and TT8::IPT1families

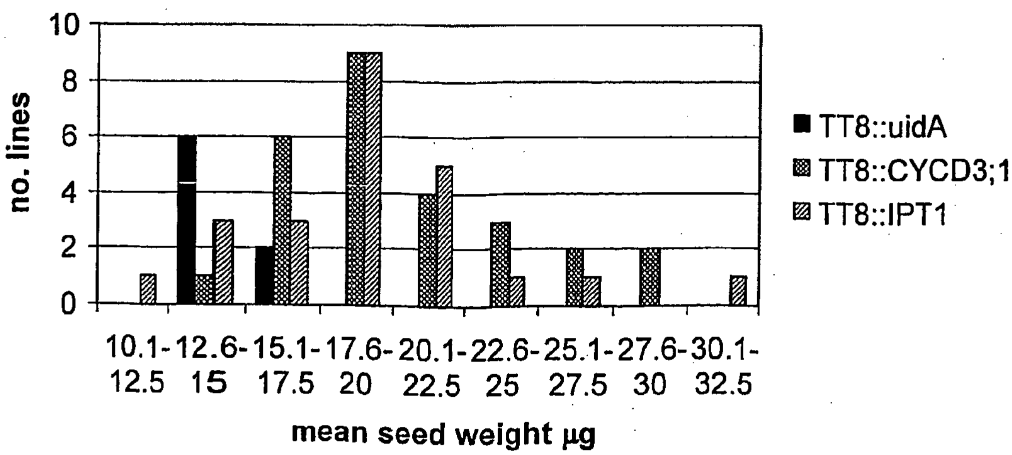
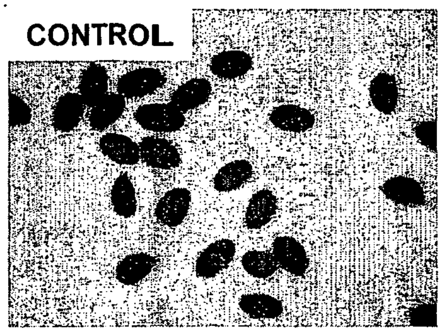
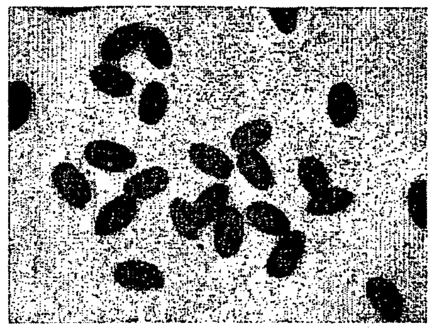


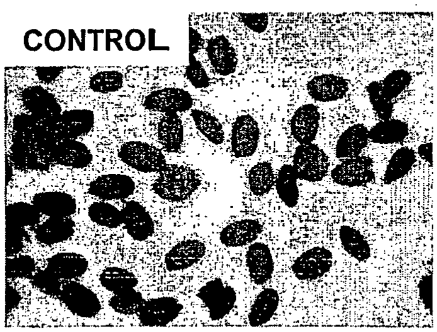
Figure 21B
Expression cassettes to increase seed size



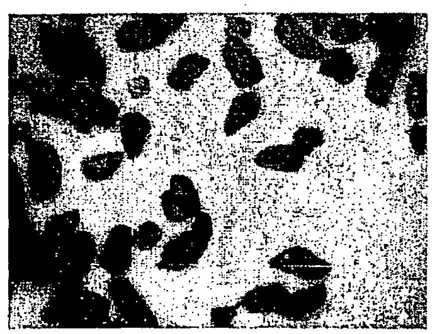
Col
mean wt 17.7 μg



BAN::CYCD3;1 line 1
mean wt 23.9 μg



Col
mean wt 15.1 μg



INO::IPT1 line 9
mean wt 23.1 μg

Figure 22
Cloning strategy, Example 14

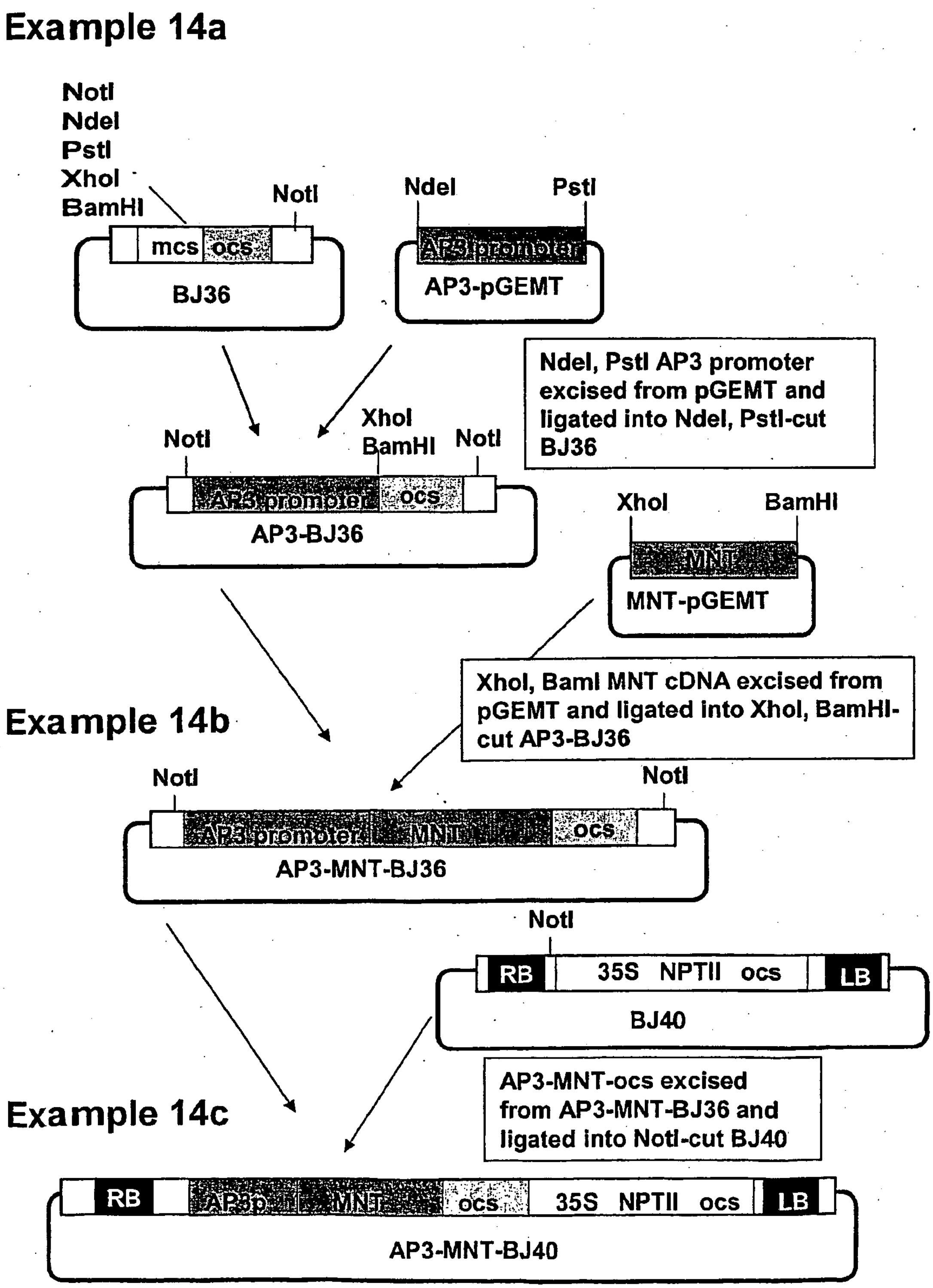


Figure 23

Cloning strategy, Example 15

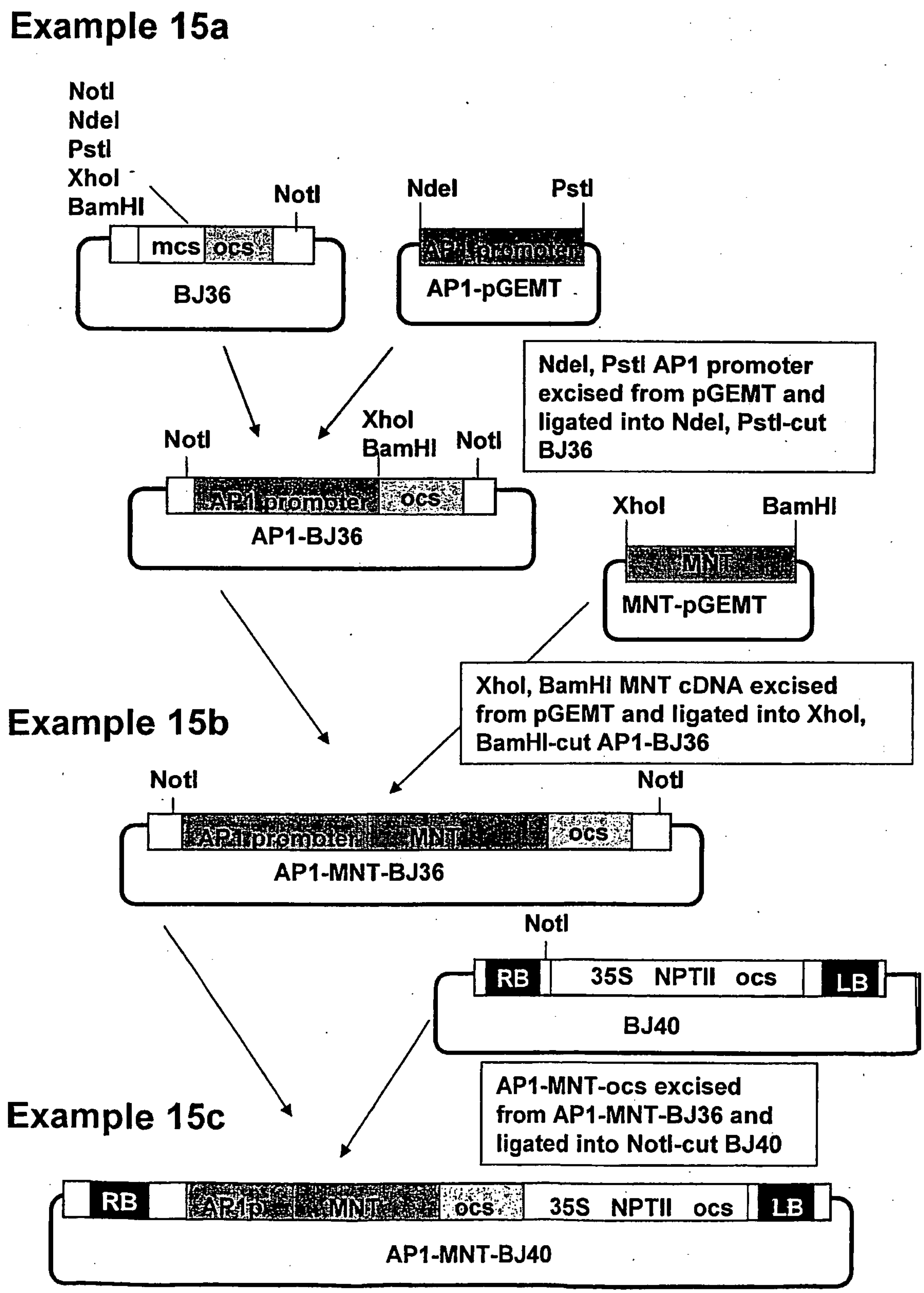
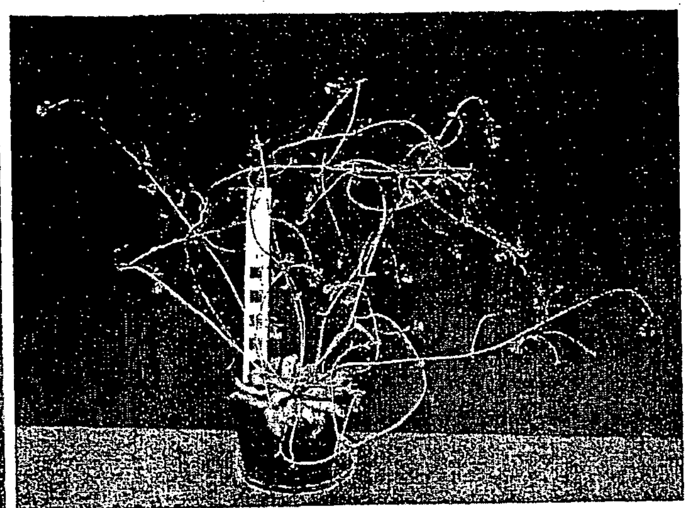


Figure 24

24A Wild-type vs *mnt-1* plants

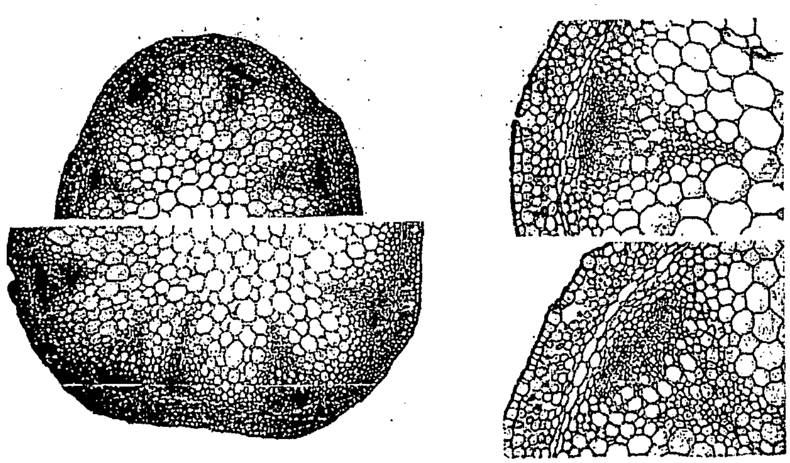


mnt-1

w.t.

24B Wild-type vs *mnt-1* stems, transverse sections

w.t.



mnt-1

Figure 25

Cloning strategy, Example 18